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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Command line parameters:

-MODEL-frame+_p2n.model -DEV-xlp
-O-/cgn2_1/USPTO_spool/US09462625/runat_07112002_101526_24854/app_query.fasta_1.327
-DB-EST -QFMY=fastap -SUFFIX-rst -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMY-pto -NORM-ext -HEAPSIZE-500 -NILEN-0 -MAXLEN-200000000
-USER-0S09462625_eCGN_1_1_2024_erunat_07112002_101526_24854 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
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Maximum DB
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Perfect score:
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1291182 UI-R-E	43 BB17	41788 GH0746	9 GH07464	z22h10	182f09	109g08 r	02830	1z23h10	196d04.r	RST6088	JI-M-AJ	ע 77652	1952cll	= :	28611	103d09	38501	AA734993 VS17h04.r	121509	AA238564 my35f04.r	82£09.x	BI556032 603237772	/35e09.	226604	02031	501771	5016690	50296	1053611	BG975104 602843369	WECA113	BG871384 602790566	T154844 5039	5774	TA53A10 6031.	2011/10/20	51956 AGE	KOOBS35 Mile miles	1650838 60329773	1149595 602848	74272 60233457	76051 xa83g01	1402	rip

ALIGNMENTS

REFERENCE AUTHORS	KEYWORDS SOURCE ORGANISM	ACCESSION VERSION	RESULT 1 AW467554/c LOCUS DEFINITION
Euratyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 575) (CI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	EST. human Homo sapiens	Similar to TR:075594 075594 PEPTIDOGLYCAN RECOGNITION PROTEIN PRECURSOR.;, mRNA sequence. AW467554 AW467554.1 GI:7037660	AW467554 575 bp mRNA linear EST 24-FEB-2000 he21d02.xl NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919651 3'

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US-09-462-625-4 (1-191) x AW467554
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Best Local Similarity:
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                                                         ProGlyAsnGlnLeuTyrHisLeuIleGlnAsnTrpProHisTyrArgSerPro 191
                                                                                                        GGAGCCCTAAGGTCCAACTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTCT
                                                                                                                           GlyAlaLeuArgSerAsnTyrValLeuLysGlyHisArgAspValGlnArgThrLeuSer 173
                                                                                                                                                                                              ValProThrProGlnAlaIleArgAlaAlaGlnGlyLeuLeuAlaCysGlyValAlaGln 153
                                                                                                                                                                                                                                                                                                                                                                                                                   AsnValGlnHisTyrHisMetLysThrLeuGlyTrpCysAspValGlyTyrAsnPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValSerHisThrAlaGlySerSerCysAsnThrProAlaSerCysGlnGlnGlnAlaArg
                                    CCAGGCAACCAGCTTTACCACCTCATCCAGAATTGGCCACANTACCGCTCCCCC
                                                                                                                                                                               GTGCCCACACCCCAGGCCATCCGGGCAGCCCAGGGTTTATTGGCCTGCGGTGTGGCTCAG
                                                                                                                                                                                                                                                   GGTCACTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAANTACATGGATCGG
                                                                                                                                                                                                                                                                        GlyHisLeuTrpAsnProMetSerIleGlyIleSerPheMetGlyAsnTyrMetAspArg
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                                                                                                                                                                                                                                                                                                                                             IleGlyGluAspGlyLeuValTyrGluGlyArgGlyTrpAsnPheThrGlyAlaHisSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -400p from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Sequencing Center Clone distribution Clone distribution: NCI-CGAP clone distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Cancer Institute, Cancer Genome Tumor Gene Index
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:2919651"
/clone_lib="WCI_CGAP_CMLI"
/clone_lib="WCI_CGAP_CMLI"
/tissue_type="myeloid cells, 18 p
rearrangement positive, includes
myeloid blast crists"
/inb_host="HHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity:
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AUTHORS
TITLE
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AW076051/c
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VERSION
KEYWORDS
SOURCE
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                                               340
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                                                                                                                                                                                                                                                                   520
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                                                                                                          AspValGlyTyrAsnPheLeuIleGlyGluAspGlyLeuValTyrGluGlyArgGlyTrp 106
                                  MetGlyAsnTyrMetAspArgValProThrProGlnAlaIleArgAlaAlaGlnGlyLeu
                                                                                                                                                                                                      SerCysGlnGlnGlnAlaArgAsnValGlnHisTyrHisMetLysThrLeuGlyTrpCys 86
                                                                                                                                                                                                                                                       CTGGCCTTACGGTATGTGGTATGGAACAGGGTGGCCAGTAGCTGCTACACCTCGCCT
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Clone distribution: WCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: I
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW076051 520 bp mRNA linear EST 13-OCT-1999 xa83901.xl NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2573424 3' similar to TR:075594 O75594 PEPTIDOGLYCAN RECOGNITION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
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National Cancer Institute, Cancer Genome Anat
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AW076051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: whole blood; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies." a 139 c 160 g 108 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:2573424"
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/tissue_type="myeloid cells, 18 pooled CML cases, BCR/ABL rearrangement positive, includes both chronic phase and myeloid blast crisis"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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US-09-462-625-4 (1-191) x BG174272
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Best Local Similarity:
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AUTHORS
TITLE
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http://image_llnl.gov
Plate: LLAMI0254 row: n column:
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Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Consc
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collecters, Park 1 (1902)
                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:4457680"
/clone_11b="NCI_CGAP_Maml"
/clone_11b="NCI_CGAP_Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
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/strain="FVB/N"
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                                                                                                                                                                                              Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.G.E. Consortium
                                                                                                                          High
                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1062 row: c column: 02
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Unpublished (1999)
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                                                                                                          quality sequence stop: Location/Qualifiers
/tissue_type="spontaneous
Stem cell origin."
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/db_xref="taxon:10090"
                           /clone="IMAGE:5011897"
/clone_lib="NCI_CGAP_Lu29"
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Sciurognathi; Muridae; Murinae; Mus
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     Eukaryota; Metazoa; Chordata; Craniata; Vert Mammalia; Eutheria; Rodentia; Sciurognathi; 1 (bases 1 to 676)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Ger
Unpublished
                                                               Mus musculus
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                                                                                               BI650838.1
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                                                                                                                     mRNA sequence.
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                                                                         house mouse.
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                                                   ArgAlaAlaGlnGlyLeuLeuAlaCysGlyValAlaGlnGlyAlaLeuArgSerAsnTyr
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Den-
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11859 row: g column: 10
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Clone distribution: MGC clone distribution information
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/dev_stage="10 months"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="IMAGE:5338401"
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                                                                            Nature 409 (6821),
                                                                                                                              and Hayashizaki,Y.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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MetLeuLeuAlaTrpAlaLeuProSerLeuLeuArgLeuGlyAlaAlaGlnGluThrGlu
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E 5 (bases 1 to 682)

Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kuriharz, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, R., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax:81-45-503-9216
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DHTGPIWNPMSIGITFMGNFMDRVPAKRALRAALNLLECGVSRGFLRSNYEVKGHRDV
QSTLSPGDQLYQVIQSWEHYRE"
                                                                                                                                                                                                                                             /note="putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAB25611.1"
/db_xref="GI:12842460"
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/strain="C57BL/6J"
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                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
Plate: LLAM14012 row: k column: 14
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AGENCOURT_8951306 NCI_CGAP_Co24
IMAGE:6474853 5', mRNA sequence
                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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                                                                                                        mRNA sequence.
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1 (bases 1 to 688)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                       Mus musculus
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                                     Eukaryota;
Mammalia; I
                                                                       house mouse
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/note="Organ: colon; Vector: pCNV-SPORT6; Site_1:
Site_2: Sal1; Cloned unidirectionally. Primer: C
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 207 c 172 g 141 t 9 others
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s musculus
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IMAGE:4485071 5',
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ValLeuLysGlyHisArgAspValGlnArgThrLeuSerProGlyAsnGlnLeuTyrHis
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                                                    CGTGCTGCCCTAAATCTTCTGGAATGTGGGGGTGTCTCGGGGGCTTCTTGAGATCCAACTAT
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Tissue Procurement: Gilbert Smith, Ph.D.
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Contact: Robert Strausberg, Ph.D.
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http://lmage.llnl.gov
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/tissue_type="tumor, biopsy sample"
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Site_2: Not1; Cloned unidirectionally. Primer: Olioso
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providing samples: Lothar Hennighausen/Robin Humphreys
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/lab_host="DH10B"
/note="0-"7
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5250362"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia D
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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11 (bases 1 to 650)
11 HadGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/dev_stage="10 months"
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                  /note-*Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 37-43 (1999). " 135 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-X
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                                                                                                                  mRNA sequence
BI154844
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Mammalia; Eutheria;
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GlnAsnTrpProHisTyrArg
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                                                                                   LysGlyHisArgAspValGlnArgThrLeuSerProGlyAsnGlnLeuTyrHisLeuIle 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NCI_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
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/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
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                   LysThrLeuGlyTrpCysAspValGlyTyrAsnPheLeuIleGlyGluAspGlyLeuVal
                                                                         TTCTGCAACAGCCCGGACTCCTGTGAACAGCAGGCCCGCAATGTGCAGCATTACCACAAG
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian
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/clone_lib="NCI_CGAP_SG2"
/clone_lib="NCI_CGAP_SG2"
/lab_host="DB10B (T1 phage-resistant)"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; S
/note="Organ: sali; Cloned unidirectionally Primer:
dT. Average insert size 1:3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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            Similarity:
                                                                                                                                                                                                                                                                                                                                          College, Northampton, Tel: 4135853826 Fax: 4135853786 Email: genome@smith.ec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA228200 627 bp mRNA linear EST 24-1 SWMFCA1124SK Brugia malayi microfilaria cDNA (SAW94LS-BmMf) malayi cDNA clone SWMFCA1124 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                               Seq
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Department of Biological Sciences, Clark
College, Northampton, MA, 01063, USA
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Unpublished (1995)
Contact: Steven A. Williams
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                                                                                                                                                                                                                                                                                                                                           genome@smith.edu
                                                                                                              /lab_host="XL1-Blue MRF'"

/note="Vector: lambda UniZap XR; Site_1: EcoR I; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from microfilariae of Brugia malayi isolated from jirds and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNASE H and DNApol I. The library had 3.5 x 1025 independent recombinants and average insert size was 900 base pairs. The library was constructed by Lori Saunders. The library is available from Dr. S.A. Williams, email
                                                                                            genome@smith.edu.
a 216 c 156
                                                                                                                                                                                                                                                        /organism="Brugia malayi"
/strain="TRS Labs"
/db_xref="taxon:6279"
/clone="SWMFCAll24"
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1 (bases 1 to 645)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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602843369F1 NCI_CGAP_Mam4
                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                               Tissue Procurement: Lothar Hennighausen
                                                                                                        CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.S.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information
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                                                                GTCATCCAACCGCTGGGAACACTACCGA
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BE199698 614 bp mRNA lir
ug52c11.x1 Barstead bowel MPLRB9 Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NCI_CGAP_Mam4"
/tlssue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
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AUTHORS
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US-09-462-625-4 (1-191) x BE199698
                   ProLeuArgTyrValValValSerHisThrAlaGlySerSerCysAsnThrProAlaSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE.Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein (MOUSE); mRNA sequence.
BE199698
BE199698.1 GI:8711867
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Location/Qualifiers
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a 159 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Barstead bowel MPLRB9"
/tissue_type="bowel"
/dev_stage="8 weeks"
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    188 TyrArg 189
              88 ValGlyTyrAsnPheLeuIleGlyGluAspGlyLeuValTyrGluGlyArgGlyTrpAsn 107.
104 TACCGA 99
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Search completed: November 12, 2002, 05:42:41 Job time: 2496 secs

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AW076051 xa83g01.x
BG187105 RST6088 A
AK008355 Mus muscu
BI453419 603170810
BG174272 602334571
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AW467554 575 bp mrNA linear EST 24-FEB-2000 he21d02.xl NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919651 3' similar to TR:075594 PEPTIDOGLYCAN RECOGNITION PROTEIN PRECURSOR: ;, mRNA sequence. AW467554 AW467554.1 GI:7037660

EST. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 575)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens namur.

Unpublished (1997)
Contact: Robert Strausberg, Ph.D. Tumor Gene Index

REFERENCE AUTHORS TITLE

SOURCE ORGANISM

ACCESSION VERSION

KEYWORDS

RESULT 1 AW467554/c DEFINITION

ALIGNMENTS

JOURNAL COMMENT

Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elisabeth Paletta, Jonathan D. Licht, M.D.,
Tissue Procurement: Blisabeth Paletta, Jonathan D. Licht, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Li
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University information can M.D., þe

Seq primer: -40UP from Gibco

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/clone_lib="NCI_CGAP_CMLI"
/tissue_type="myeloid cells, 18 pooled CML cases, BCR/ABL rearrangement positive, includes both chronic phase and myeloid blast crisis"
/lata_self="PHIOB"
/lata_self="PHIOB"
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147 c 178 g 135 t 5 others
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/db_xref="taxon:9606"
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                                                                   520 bp mRNA
Homo sapiens cDNA
594 PEPTIDOGLYCAN F
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206 CTGCCCTTACGCTATGTGGTGGTATCGCACACGGCGGCAGCAGCAGCTGCAACACCCCCGCC 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Li Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 252.
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1 (bases 1 to 520)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
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/clone="mmAGE:2573424"
/clone_lib="NCI_CGAP_CML1"
/clsue_type="myeloid cells, 18 poorearrangement positive, includes bomyeloid blast crisis"
/lab_host="DH10B"
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Creation of genome-wide protein expression libraries using random
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: 216 431 9900
: 216 361 9596
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quality sequence stop
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139 c 95 g 81 t 1 others
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/cell_line="HT1080"
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/db_xref="taxon:9606"
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                                                                                                   Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new common Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (strain:C57BL/6J) adult male : mRNA, clone_lib:RIKEN full-length enriched clone:2010107E11
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682 bp mRNA linear HTC 19-JAN-Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010107E11:peptidoglycan recognition
                                                           Functional annotation of a Nature 409 (6821), 685-690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253
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Kohtsuki, S

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                   CCTGCTGCAGCCCCATAGTGCCCCGGAACGAGTGGAAGGCCCCTGGCATCAGAGTGCGCCC 194
                                                                                             CCTCCTGCAGTTTCATCGTGCCCCGCAGTGAGTGGAGGGCCCTGCCATCCGAGTGCTCTA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web site (http://genome.gsc.riken.go.jp/)
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                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAB25611.1"
/db_xref="GI:12842460"
/db_xref="MGI:12842460"
/db_xref="MGI:1345092"
/translation="MLFACALIGIATSCSFIVPRSEWRALPSECSSRLGHPVRYV
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VISHTAGSFCNSPDSCOGQARNVQHYHKNELGWCDVAXNFLIGEDGHYYEGRGWNIKG
DHTGPIWNPMSIGITFMGNFMDRVPAKRALRAALNILLECGVSRGFLRSNYEVKGHRDV
QSTLSPGDQLYQVIQSWEHYRE"
                                                                                                                                                                                                                                                                                                                     /gene="Pglyrp"
/note="putative"
682
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putative*
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/db_xxef="FaNTOM_DB:2010107E11"
/db_xxef="MGD:MGI:1910652"
/db_xxef="taxon:10090"
/clone="2010107E11"
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                                                                                                                                                                                                                                                             /note="putative"
217 c 175 g
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                /gene="Pglyrp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="data source:MGD,
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                                                                                                                                                                                     44.18;
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NIH-MGC http://mgc.nci.nih.gov/.
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                   163
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humph:
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                  /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Se
Site_2: NotI; Cloned unidirectionally. Primer: Oligo
Library constructed by Life Technologies. Investigator
                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:5250362"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
Lothar Hennighausen/Robin Humphrevs.
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                                                                                                                                                                                                                                                                                          mRNA sequence.
BG174272
BG174272.1 GI
                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
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/organism="Mus musculus"
/strain="FVB/N"
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Mammalia; Eutheria; Rodentia; Sciurognathi;

1 (bases 1 to 610)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Ge

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                          mRNA sequence.
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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/dev_stage="10 months, virgin"
/lab_host="DH10B"
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Pred. No. 2.9e-63;
0; Mismatches 115;
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Sciurognathi; Muridae;
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IMAGE:5032278 5',
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Murinae; Mus
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Ph.D.,

Chu-Xia Deng Ph.D

FEATURES

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Query Match
Best Local Similarity
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11090 row: d column: 07
High quality sequence stop: 610.
                      BI149595 (602848402F1 NCI_CGAP_Lu29
      mRNA sequence.
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/dev_stage="10 months"
/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Mam3"
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/db_xref="taxon:10090"
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AAGGACACCGGGATGTGCAGCGTACACTCTCTCCAGGCAACCAGCTCTACCACCTCATCC
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                                                                              CCCAGGGTCTACTGGCCTGCGGTGTGGCTCAGGGAGCCCTGAGGTCCAACTATGTGCTCA
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Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 637)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMI1062 row: c column: 02
High quality sequence stop: 632.
Location/Qualifiers
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Tissue Procurement: Gilbert Smith,
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Contact: Robert Strausberg, Ph.D
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a 196 c 167 g 137 t
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/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5011897"
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TGGCTGGTGCGATGTAGCCTACAACTTCCTTATTGGAGAGGACGGTCATGTCTATGAAG
                                                                                                                                    AGCACCTGAGCCTGCCCTTACGCTATGTGGTGGTATCGCACACGGCGGCAGCAGCAGCTGCA
                                                                                                                                                                                                     CCTCCTGCAGTTTCATCGTGCCCCCGCAGTGAGTGGAGGGCCCTGCCATCCGAGTGCTCTA 173
                     TGGGCTGGTGCGACGTGGGCTACAACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGG
                                                                  ACAGCCCGGACTCCTGTGAACAGCAGGCCCGCAATGTGCAGCATTACCACAAGAATGAGC
                                                                                    ACACCCCCCCCTCCTCCAGCAGCAGCAGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://image.llnl.gov
http://image.llnl.gov
Plate: LLAM11094 row: f column: 12
High quality sequence stop: 637.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
BI155774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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Clone distribution: MGC clone distribution information can
Cound through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                       /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."
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/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
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/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5033867"
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                                                                                                                                                                                                                                                                         Score 315; DB 13;
Pred. No. 3e-63;
0; Mismatches 115;
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Mus musculus
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135 CCTGCTGCAGCCCCATAGTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCC 194

Query Match Best Local

Local Sinthes 384;

Similarity

43.9%; 77.0%;

Score 315; DB 1 Pred. No. 3e-63; 0; Mismatches 1

115;

0;

Gaps

0

DB 13;

Length 676; Indels

Conservative

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REFERENCE
AUTHORS
TITLE
BASE COUNT
ORIGIN
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ORGANISM
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11859 row: g column: 10
                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-x
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                156
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       /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 37-43 (1999)."
                                                                                                                                /clone="IMAGE:5338401"
/clone_lib="NCI_CGAP_MAm3"
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/dev_stage="10 months"
/lab_host="DH10B"
                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
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IMAGE:5338401 5',
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; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;

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/db_xref="taxon:10000"
/clone="IMAGE:6474853"
/clone=lib="NCI_CGAP_CC24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo d:
Average insert size 1.6 kb. Constructed by Life
                                                                                                                                                                             /strain="FVB/N"
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                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10326 row: c column: 24
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1 (bases 1 to 688)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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 f Mus musculus
Eukaryota; Metazoa; Chordata; Cran
Mammalia; Eutheria; Rodentia; Sciu
1 (bases 1 to 842)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mam
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGCTGGTGCGACGTGGGCTACAACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGG
                                                                                                                                                                                                                                                AGAATTGGCCACACTACCG 633
                                                                                                                                                                                                                                                                                  AAGGACACCGGGATGTGCAAAGCACTCTCTCTCCAGGTGACCAACTCTATCAGGTCATCC
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                                                                                                                                                                                                                                                                                                                                  CCCTAAATCTTCTGGAATGTGGGGTGTCTCGGGGGCTTCTTGAGATCCAACTATGAAGTCA
                                                                                                                               mRNA sequence.
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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4485071"
/clone=lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="bH10B"
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a 209 c 180 g 142 t
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77.08;
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Pred. No. 3e-63;
0; Mismatches 1
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Sciurognathi; Muridae;
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IMAGE:5117688 5',
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ACACCCCCCCCTCGTGCCAGCAGCAGCCAGGCCCGGAATGTGCAGCACTACCACATGAAGACAC
                                  http://image.llnl.gov
http://image.llnl.gov
Plate: LLAM11286 row: k column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cyapbs r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
CDNA Library Preparation: M. Bento
                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by:Incyte Genomics, Inc. Clone distribution: NCI-CGAP clone distribution inf found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                  Conservative
                                                                                                                                                                                   quality sequence stop: :
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus
/strain="CZECH
                                                                                                                                           43.8%;
                                                                                                                                0
                                                                                                                                          Score 314.6; DB 1 Pred. No. 3.8e-63;
                                                                                                                                                                                                                                                                                                                                                                                          musculus"
                                                                                                                                Mismatches 116;
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                                                                                                                                                                                                                                                                                    48
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                                                                                                                                          GCAACACCCCCGCCTCGTGCCAGCAGCAGCCCGGAATGTGCAGCACTACCACATGAAGA 311
                                                                                                                                                                                                                                                                                                                                                             391;
                                                            CACTGGGCTGGTGCGACGTGGGCTACAACTTCCTGATTGGAGAAGACGGGCTCGTATACG
                                                                                                                                                                                                                       CCCAGCACCTGAGCCTGCCCTTACGCTATGTGGTGGTATCGCACACGGCGGCAGCAGCAGCT
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  AGGGCCGTGGCTGGAACTTCACGGGTGCCCACTCAGGTCACTTATGGAACCCCATGTCCA 431
                                                                                                                       GCACCAGCCCAGCCTCCTGCGAGCAGCAGCATCGCAATGTGCAGCATTACCACATGAGCT
                                                                                                                                                                                                  Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
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SWMFCAL1124SK Brugia malayi microfilaria cDNA (SAW94LS-BmMf)
malayi cDNA clone SWMFCA1124 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 4135853826
Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith College Department of Biological Sciences Department of Biological Sciences, Clark Scienc College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes expressed in microfilaria
Unpublished (1995)
Contact: Steven A. Williams
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AA228200
AA228200.1 GI:1849758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome@smith.edu."
a 216 c 156 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note "Vector: lambda Unizap XR; Site_1: EcoR I; Site_2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from microfilariae of Brugia malayi isolated from jirds and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNApol I. The library had 3.5 x 10E5 independent recombinants and average insert size was 900 base pairs. The library was constructed by Lori Saunders. The librarith cd. "allable from Dr. S.A. Williams, email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Brugia malayi"
/strain="TRS Labs"
/db_xref="taxon:6279"
/clone="SWMFCA1124"
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Gaps

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CCTCCTGCAGTTTCATCGTGCCCCGCAGTGAGTGGAGGGCCCCTGCCATCCGAGTGCTCTA 168

Matches

Similarity

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JOURNAL COMMENT
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAN10976 row: j column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 645)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria;
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                                                                                /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall Site_2: NotI; Cloned unidirectionally. Primer: Oligo di Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Grov and Differentiation 7, 3-11 (1996)."
                                                                                                                                                                                                /tissue_type="tumor, gross tissue"
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                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="IMAGE:4979057"
/clone_lib="NCI_CGAP_Mam4"
                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="NMRI"
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               42.7%;
77.3%;
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Rodentia;
Score 306.6; DB 13;
Pred. No. 2.7e-61;
); Mismatches 109;
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Search completed: November 12, 2002, 02:17:56 Job time: 2478 secs

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Copyright (c) 1993 - 2002 Compugen Ltd.
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SUMMARIES

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ALIGNMENTS

REFERENCE AUTHORS TITLE VERSION
KEYWORDS
SOURCE
ORGANISM RESULT 1
AF242517
LOCUS
DEFINITION
ACCESSION AF242517 724 bp mRNA linear PRI 15-AUG-2000 Homo sapiens hypothetical protein SBBI68 mRNA, complete cds. AF242517 AF242517.1 GI:9802032 Homo sapiens.

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 724)
1 (bases 1 to 724)
Wan,T., Zhang,W. and Cao,x.
Direct Submission
Submitted (08-MAR-2000) Department of Immunology, Second Military

JOURNAL

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                                      CCCCACTGTCTCCTTCTCCAATAAAGATG
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ECAQHLSLPLRYVVSHTAGSSCNTPASCQQARNVQHYHMKTLGWCDVGYNFLIGED
GLVYEGRGWNFTGAHSGHLWNPMSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGA
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251 c 186 g 126 t
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Kang,D., Liu,G., Lu
Direct Submission
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A peptidoglycan recognition protein in innate immunity conserved from insects to humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens peptidoglycan mRNA, complete cds.
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1 (bases 1 to 690)
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96.7%;
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1 (bases 1 to 700)
Kappeler, S. R., Farah, Z. and Puhan, Z.
Milk as a Source of Camel (Camelus dromedarius)
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/rodon_start=1
/protein_id="CAC1953.1"
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/protein_id="CAC1953.1"
/db_xref="GI:11990124"
/translation="MTRHCVLLVWALLALLSLGAAREDPPACGSIVPRREWRALASEC
/translation="MTRHCVLLVWALLASEC"
/translation="MTRHCVLLVWALL
                                                                        /product="peptidoglycan recognition 678..683
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                                                                                                                                                                                                                                                                                                               /sub_species="Somali
/db_xref="taxon:9838"
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2 (bases 1 to 688)
Yount, N.Y., Yuan, J., Tydell, C.C. ar
Direct Submission
Submitted (11-MAR-2002) Pathology,
1, Irvine, CA 92697, USA
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1 (bases 1 to 688)

1 (bases 1 to 688)

Tydell,C.C., Yount,N., Tran,D., Yuan,J. and Selsted,M.E.
Tsolation, characterization, and antimicrobial propertie
oligosaccharide-binding protein. A microbicidal granule
eosinophils and neutrophils
J. Biol. Chem. 277 (22), 19658-19664 (2002)
                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                   Bovidae; Bovinae; Bos.
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Eutheria; Cetartiodactyla; Ruminantia; Pecora;
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                                                     GCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCCTGAGGCCCTG
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           CTGATCCGCACCCCATTCCTCCCCTCCCAAAAAACCCCCACTGTCTCCTTCTCCAA
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order(146. 148,281. 283)
/note="disulfide bond"
order(209. 211,227. 229)
/note="disulfide bond"
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cyclization; peptidoglycan recognition protein;
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RQPVRYVVVSHTAGSVCNTPASCQRQAQNVQYYHVRERGWCDVGYNFLIGEDGLVYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="oligosaccharide-binding
/protein_id="AAL87002.1"
/db_xref="GI:19550242"
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/cell_type="periphera
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Pred. No. 9.4e-68;
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1 (bases 1 to 549)

1 (bases 1 to 549)

Georgiev,G.P., Kiselev,S.L., Prokhorche Nucleic acid encoding tag7 polypeptide Patent: US 6172211-A 1 09-JAN-2001;
Location/Qualifiers
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                                                                               AAGGACACCGGGATGTGCAGCGTACACTCTCTCCCAGGCAACCAGCTCTACCACCTCATCC 614
                                                                                                                                              CCCAGGGTCTACTGGCCTGCGGTGTGGCTCAGGGAGCCCTGAGGTCCAACTATGTGCTCA 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (11-OCT-1999) Pediatrics, University of Utah, 50 North Medical Drive, Room 2A126, Salt Lake City, UT 84132, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 669)
Slayton, W.B., Rigaa, A.,
Trautman, M.S., Spangrude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Slayton, W.B., Rigaa, A., Hancock, J.D., Zaugg, J.K., Le, T.V., Trautman, M.S., Spangrude, G.J., Carroll, W.L. and Schibler, K.R. Granulocyte-colony stimulating factor up-regulates expression murine tag7 during myeloid differentiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="TAG7-11ke protein"
/protein_id="AAF06335.1"
/protein_id="AAF06335.1"
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VISHTAGSPCNSPDSCEQQARNVQHYHKNELGWCDVAYNFLIGEDGHVYEGRGWNIKG
DHfGPIWNPMSIGITEMGNFWDRVPAKRALRAALNLLECGVSRGFLRSNYEVKGHRDV
QSTLSPGDDQLYQVIQSWEHYRE"
QSTLSPGDDQLYQVIQSWEHYRE"
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/db_xref="taxon:10090"
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/cell_line="32D cl3"
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77.28;
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Spangrude, G.J., Carroll, W.L. and Schibler, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               type-"myeloblast"
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Pred. No. 1.9e-60;
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GCCGTGGCTGGAACTTCACGGGTGCCCACTCAGGTCACTTATGGAACCCCCATGTCCATTG
                                                                                                                                     TGGGCTGGTGCGACGTGGGCTACAACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGG
                                                                              ACAGCCCGGACTCCTGTGAACAGCAGGCCCGCAATGTGCAGCATTACCACAAGAATGAGC
                                                                                            ACACCCCCGCCTCGTGCCAGCAGCAGCAGCGGGAATGTGCAGCACCTACCACATGAAGACAC
                        TGGGCTGGTGCGATGTAGCCTACAACTTCCTTATTGGAGAGGACGGTCATGTCTATGAAG
                                                                                                                                                                AGCACCTGAGCCTGCCCTTACGCTATGTGGTGGTATCGCACACGGCGGCAGCAGCTGCA 254
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Submitted (08-JUL-1998) Microbiology,
Stockholm S-106 91, Sweden
Location/Qualifiers
680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A peptidoglycan recognition protein in innate immunity conserved from insects to humans

Proc. Natl. Acad. Sci. U.S.A. Os / 77.
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19,D., Liu,G., Lu
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/product="peptidoglycan recognition
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84. .581
                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MLFACALLALIGLATSCSFIVPRSEWRALPSECSSRLGHPVRYVVISHTAGSFCNSPDSCEQQARNVQHYHKNELGWCDVAYNFLIGEDGHVYEGRGWNIKGDHTGFIWNPASIGITEWGNFWDRVPAKRALRAALNLLECGVSRGFLRSNYEVKGHRDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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/db_xref="GI:3342531"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="spleen"
1. .680
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/note="PGRP"
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/db_xref="taxon:10090"
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Pred. No. 1.9e-60;
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Mus musculus, pe
IMAGE:3969014, n
                                                                                                                                                                                                      Clone distribution: MGC clone distribution informat through the I.M.A.G.E. Consortium/LLNIL at: http://i Series: IRAK Plate: 17 Row: j Column: 22 This clone was selected for full length sequencing passed the following selection criteria: matched mf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC005582
BC005582.1
MGC
                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
DNA Sequencing by: Baylor College of Medicine Human
Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                             Gunaratne, P.H., Garcia, A.M., Lu, Yoon, V.S., Kowis, C.R., Lawrence, Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Mammalia; Eutheria;
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                                                                                               model.
                                                                                                                                    /organism="Mus musculus"
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       /codon_start=1
/product="peptidoglycan
                                                                //tlssue_type="Mammary tumor. Meta
model. 10 month old virgin mouse.
/clone_1lb="NCI_CGAP_Mam1"
/lab_host="DH10B"
                                                                                                         /tissue_type="
                                                                                                                     /clone="MGC:11430 IMAGE:3969014"
                                                                                                                                                                                             Location/Qualifiers
                                                  note="Vector:
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       protein"
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                                                                      Eukaryota; Metazoa; Chordata; Crania; Mammalia; Eutheria; Rodentia; Sciuro; 1 (bases 1 to 678)
Kustikova,O.S., Kiselev,S.L., Borodu; Afanas'eva,A.V. and Kabishev,A.A.
Cloning of the tag7 gene expressed in Genetika 32 (5), 621-628 (1996)
                                                                                                                                                                                                                                                                                                                                               AAAGCTGGGAACACTACCG
                                                                                                                                                                                                                                                                                                                                                                         AGAATTGGCCACACTACCG 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCTAAATCTTCTGGAATGTGGGGTGTCTCGGGGGCTTCTTGAGATCCAACTATGAAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCATCACCTTCATGGGGAACTTCATGGACCGGGTACCCGCAAAGCGGGCCCTCCGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCGAGGCTGGAACATCAAGGGTGACCACACAGGGCCCATCTGGAATCCCATGTCTATTG
 Direct Submission
Submitted (18-APR-1995)
                            2 (bases 1 to 678)
Kustikova, O.S.
                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                                              M.musculus mRNA for TAG7
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  Kustikova,
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//db_xrefi="GI:13542756"
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135 CCTGCTGCAGCCCCATAGTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCC 194
                                                AGCACCTGAGCCTGCCCTTACGCTATGTGGTGGTATCGCACACGGCGGCAGCAGCAGCTGCA 254
                                                                                                                                           CCTCCTGCAGTTTCATCGTGCCCCGCAGTGAGTGGAGGGCCCCTGCCATCCGAGTGCTCTA 149
314
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TGGGCTGGTGCGACGTGGGCTACAACTTCCTGATTGGAGAAGACGCGCCTCGTATACGAGG ACACCCCCGCCTCGTGCCAGCAGCAGGCGCGGAATGTGCAGCACTACCACATGAAGACAC 374 329 269

GCCGTGGCTGGAACTTCACGGGTGCCCACTCAGGTCACTTATGGAACCCCATGTCCATTG 434 389

GCATCAGCTTCATGGGCAACTACATGGATCGGGTGCCCACACCCCCAGGCCATCCGGGCAG 449 494

CCCAGGGTCTACTGGCCTGCGGTGTGGGCTCAGGGAGCCCTGAGGTCCAACTATGTGCTCA 554

AAGGACACCGGGATGTGCAAAGCACTCTCTCTCCAGGTGACCAACTCTATCAGGTCATCC AAGGACACCGGGATGTGCAGCGTACACTCTCTCCAGGCAACCAGCTCTACCACCTCATCC 614

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Senin, V.M., mouse tumors

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                                                                        AAGGACACCGGGATGTGCAGCGTACACTCTCTCCAGGCAACCAGCTCTACCACCTCATCC 614
                                                                                                                        CCCAGGGTCTACTGGCCTGCGGTGTGGCTCAGGGAGCCCTGAGGTCCAACTATGTGCTCA 554
                                                                                                                                                              GCATCACCTTCATGGGGAACTTCATGGACCGGGTACGCAAA - -GCGGGCCCCTCCGTGCTG
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                                                                                                                                                                                                                                                                                                    TGGGCTGGTGCGACGTGGGCTACAACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGG
                           AGAATTGGCCACACTACCG 633
                                                    AAGGACACCGGGATGTGCAAAGCACTCTCTCTCCAGGTGACCAACTCTATCAGGTCATCC
                                                                                                         CCCTAAATCTTCTGGAATCTGGGGGTGTCTCGGGGGCTTCCTGAGATCCAACTATGAAGTCA
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Kabishev,A.A., Lukanidin,E.M. and Georgiev,G.P.
Molecular cloning and characterization of the mouse tag7 gene
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a 216 c 173 g 143 t
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36. .491
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/dev_stage="adult"
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/strain="A/Sn"
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Lamerdin, J.E.
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Submitted (11 JUN-1999) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from q centromere to telomere. BAC 282485 overlaps cosmid R30477 to the left from bases 1 to 4,419 of this accession, and overlaps BAC 264576 (CIT-B-297N14; AC006262) from accession, and overlaps BAC 264576 (CIT-B-297N14; AC006262) from bases 146,203 to 166,500. Additional chromosome 19 map and sequence information may be obtained at:

information may be obtained at:

Location/Qualifiers
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ELGRLQGLDGQNTRDTRENEIWHLREQVSRLASEKRELEAQLGRSREBALAGRAARQE
AEALRGLVRGLELELRQERGLGHRYAGRRGQDCRRLAKELEEAKASERSLRARLKTLT
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/codon start=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Hypothétical arginine-rich gene product; Hypothetical CDS constructed from overlapping ESTs and Xgrail predictions. EST coverage is lacking for some portions of the CDS. Gene may be alternatively spliced, a multiple transcripts map into this region; alternatively, these individual clones may represent artifactual events.
                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=3
/evidence=not_experimental
/product="BC282485_1"
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12784. .12994,13080. .13162,13903. .13958,14053. .14128,
14429. .14568,14726. .14804,14982. .15039,15813. .15885,
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/clone_lib-"Cal Tech CIT-B BAC library"
/note="LLNL clone name: BC282485"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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chromosome 19, BAC
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misc_feature

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/note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 100.000"
complement(6148. .6443)
                                                                                                                                                                                                                                            /note-"DDS similarity to overlapping ESTs:
N39722 yx92e04.rl Homo sapiens cDNA clone 269214 5';
(439. .506); 71% identity. -AA143160 z149d07.rl Soares
pregnant uterus NbHPU Homo sapiens cDNA clone 505261 5';
(282. .379); 100% identity. -AA142881 z149d07.sl Soares
pregnant uterus NbHPU Homo sapiens cDNA clone 505261 3';
(274. .175); 95% identity."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="AluSg/x"
complement(2747. .3044)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="Alusx"
5875. .5972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=DDS similarity to overlapping ESTs:
//1016=DDS similarity to overlapping ESTs:
//10256.438); 81% identity-AA283147 zt14d07.r1
//10256.438); 81% identity-AA283147 zt14d07.r1
//10256.1021 Homo sapiens cDNA
//10256.1021 Clone IMAGE:713101 5'; (248.400); 99% identity-AA143160
//10256.1021 Clone IMAGE:713101 5'; (248.400); 99% identity-AA143160
//10256.1021 Clone Sobject CDNA
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                                                                                                                                                          /note="DDS similarity to N28707 yx66d11.r1 Homo sapiens CDNA clone 266709 5'; (223. .246); 100% identity."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zl49d07.rl Soares pregnant uterus kibHPU Homo sapiens cDNA clone 505261 5'; (44. .126); 100% identity.-N28707 yx66d11.rl Homo sapiens cDNA clone 266709 5'; (1. .66); 98% identity.-AA142881 zl49d07.sl Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505261 3'; (526. .438); 82%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-*DDS similarity to overlapping ESTs:
/N39722 yx92e04.rl Homo sapiens cDNA clone 269214 5';
(12. .170); 99% identity.-AA283147 zt14d07.rl NCI_CGAP_GCB1
Homo sapiens cDNA clone IMAGE:713101 5'; (6. .163); 99%
identity.-AA143160 z149d07.rl Soares pregnant uterus NbHPU
Homo sapiens cDNA clone 505261 5'; (1. .43); 100%
identity.-AA142881 z149d07.sl Soares pregnant uterus NbHPU
Homo sapiens cDNA clone 505261 3'; (570. .527); 64%
                                rpt_family="Alusx"
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complement/2000
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complement/coro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="Alusx"
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EDFSESLSRGGHRRRGKPPSPTPWSGSNMKSPPVERSHHQKSLANSGGWVPIKEYSSE
HQAADMAEIDARLKALQEYMNRLDMRS"
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frame: 0, quality: good, score:
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. .3750
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GACCCGGCCTGCTGCAGCCCCATAGTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAG 187
                                                                                                              ATGCTGCTTGCCTCGGCTCTCCCCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAA 127
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                                                                                                                                                                                                                                                                                                                                                     314;
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                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(13799. .13954)
/rpt_family="GC_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="predicted exon, program: grail2exons_human_1.3, frame: 2, quality: excellent, score: 100.000-DDS similarity to AA765166 nz79c05.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1301672; (122. .48); 100%
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complement(11914. .11976)
/rpt_family="AT_rich"
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complement(12186. .12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identity."
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complement/1000
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complement/incr
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complement(11864. .11
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11322. 11610
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complement(10587...10752)
/rpt_family="AluJ"
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frame: 1, quality: excellent, score: 92.000"
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complement/11077
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9456. .952
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.3080. .13162
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11775. .11814
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complement/0700
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complement/7700
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92.6%;
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                                                                                                                                                                                                                                                                                                                                                                   Score 299; DB 9;
Pred. No. 8.3e-57;
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                        GCAACACCCCCCCCTCCTGCCAGCAGCAGCCCCGGAATGTGCAGCACTACCACATGAAGA 311
                                                                                                     GCAGCAGCCCAGACTCCTGTGAACAGCAGCCCCGCAATGTGCAGCTTTACCAAATGAAAC
                                                   AGCTGCAACACCCCCGCCTCGTGCCAGCAGCAGCAGCCCGGAATGTGCAGCACTACCACATG
                                                                                                                                                                al Similarity
373; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pharmacology, and Physiology, Washington State University, 646520, Pullman, WA 99164, USA
LOcation / Washington State University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rehman, A., Teodecki, E.E. and Krueger, J.M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
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Rattus norvegicus peptidoglycan
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                                                                                                                                                                                                                                 134
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                                                                                                                                                                                                                                ω
                                                                                                                                                                                                                         /Product="peptidoglycan recognition protein pgrp"
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GDHTGFIWNPMSIGITFMGDYREP"
VQSTLSPGDQXYEIQGSWDHYREP
VQSTLSPGDQXYEIQGSWDHYREP
193 c 166 g 137 t
                                                                                                                                                                                                                                                                                                                                          /note="similar to Homo sapiens and peptidoglycan recognition protein; ni and Mus musculus TAG7"
                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Pgrp"
20. .571
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="spleen"
1. .630
                                                                                                                                                                                                                                                                                                                                                                                       /gene="Pgrp"
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                                                                                                                                                                        41.2%;
                                                                                                                                                             0;
                                                                                                                                                         Score 295.6; DB 1
Pred. No. 9.4e-56;
0; Mismatches 129
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n protein PGRP (Pgrp)
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                                                                                                                                                                                   Length
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423 CTGCCCTAAATCTTCTGAAATGTGGGGTGTCTGAGGGCCTTCCTGAGATCTAACTATGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAAAGGACATCGAGATGTGCAAAGCACTCTGTCTCCAGGTGACCAGCTCTACGAGATCA
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                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (06-APR-2001) Kappeler
Institute of Technology, Zurich,
SWITZERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The peptidoglycan recognition protein, lactating mammary gland of camels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa partial mRNA for p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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AJ310355
                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 259)
                                                            47
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/product="peptidoglycan recognition
86 c 83 g 43 t
                                                                                                                                                                                                                                /gene="pglyrp"
<2. .>259
                                                                                                                                                                                        /gene="pglyrp"
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                                                                                                                                                                                     /codon_start=1
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/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                          country="Switzerland"
                                                                                                                                                                                                                                                                                        /tissue_type="adipose"
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26, ETHZ, CH-8092 Zurich,
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82. . 28

Score 185.4; DB 4; Pred. No. 3.9e-31;

Length

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGGCTTGTGTATGAAGGCCGGGGCTGGAACACCGTGGGCGCCACTCAGGTCCCACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCGGGCACCTGCGATAACCCGGCCTCATGCCGGCGTCAGGTCCAGAACGTGCAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Camelus dromedarius pgrp gene for peptidoglycan recognition protein, flanking region and exons 1-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-MAR-2001) Kappeler S.R., Food Science, Swiss Federal Institute of Technology, Zurich, LFO F26, ETHZ, CH-8092 Zurich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kappeler, S.R., Farah, Z. and Puhan, Z.

The peptidoglycan recognition protein is expressed in the lactating mammary gland of camels and binds to lactic acid bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Camelus dromedarius
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kappeler, S.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptidoglycan recognition protein; pgrp gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
   /gene="pgrp"
1585. 11590
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898. .1063
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203. .210
                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9838"
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/country="United Arab Emirates"
/note="breed Arabian"
                                                                                                                                                                                                                                                                                                                                                                                               organism="Camelus dromedarius"
                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                     rpt_family="SINE/MIR"
585. .5358
                                                                                                                                                                                                  note="similar AF217601"
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join(1641. 1921,4528. .4649,5086. .5264)
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/protein_id="CAC84130.1"
/db_xref="GI:17939893"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="binding to bacterial peptioglycan (low
pross-linked and low-modified)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kin, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snit, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence and relationship to other sequences, please visit our sequence
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Direct Submission
Submitted (16-MAR-1999) Drosophila Genome Center, Lawrence Submitted (18-MAR-121, Berkeley, CA 94720, USA CA 94720, USA On Mar 17, 2001 this sequence version replaced gi:5670628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
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On Mar 17, 2001 this s
Sequence submitted by:
Berkeley Drosophila Ge
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/clone=lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
pBACe3.6)"
36967 c 36753 g 46416 t
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                     RS Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galler, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibeywam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheler, F., Stapletton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C. Sequencing of Drosophila chromosome 2R, region 44E-44F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGCCGCCCAGCAGCTGCTCAACGACGCCGTCAACCGTGGCCAGCTCAGCTCCGGCTACA 152476
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Best Local Similarity 57.3
Matches 287; Conservative
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JOURNAL
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                                                                                                                        TGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTCTCCAGGCAACCAGCTCTACCACC 608
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                                                                                      TCCTGTACGGTCATCGCCAGGTCAGCGCCACCGAATGCCCCGGCACCCACATCTGGAACG 11266
                                               TCATCCAGAATTGGCCACACT 629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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/Clone=1ib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
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a 38440 c 38294 g 46671 t
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
/chromosome="2R"
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Search completed: November 12, 2002, 01:40:58 Job time: 2994 secs

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Command line parameters:

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40: em_htgo_nus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result 00 C ŏ 405.5 403.5 395.5 388.5 388.5 379 379 369 369 369 368 348.5 348.5 348.5 650.5 650.5 505.5 505.5 441 414.5 414.5 414.5 Score Query Match 1000 Length DB AX119920 AX119917 BC019396 AC014935 AC006933 AF313391 AB016249 AB017520 AF242518 AF076481 SSC310355 AY035377 AF207542 AY060645 AE003836 AX119918 AX119915 AC007303 AC020451 AF193843 AF076482 BC005582 H AX1155-AX035377 Homo S., AF207542 Drosophil AY060645 Drosophil AY060645 Homo sapi AR124884 Sequence AF193843 Mus muscu AF076482 Mus muscu BC005582 Mus muscu BC005582 Mus muscu AF154114 Rattus no X86374 M.musculus AC007785 Homo sapi AC007785 Drosophil AC007303 Drosophil AC007311 Drosophil AX119920 Sequence AX119917 Sequence BC019396 Mus muscu AC014935 Drosophil AC006933 Drosophil AC010688 Drosophil AC003526 Drosophil AF076481 Trichoplu AJ310355 Sus scrof AF207541 Drosophil AY075293 Drosophil AF441723 Bombyx mo AJ409286 Camelus d AF500096 Drosophil AF384856 Homo sapi E16480 Bombyx mori E16479 Bombyx mori AK055882 Homo sapi AK055882 Homo sapi AK055882 Homo sapi AK055882 Homosphil AF313391 Drosophil AF076483 Homo sapi AF242517 Homo sapi AJ131676 Camelus d AY083309 Bos tauru AB016249 Bombyx mo AB017520 Bombyx mo AE003836 Drosophil Description 8 Sequence 5 Sequence 7 Homo sapi

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mRNA, complete
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Direct Submission
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A peptidoglycan recognition protein in innate immunity conserved from insects to humans
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Direct Submission
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Submitted (21-DEC-1998) Kappeler S.R.,
Swiss Federal Institute of Technology,
                                                                                                                                                                                                                                            peptidoglycan recognition protein.
Arabian camel.
Camelus dromedarius
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
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Kappeler, S.R., Farah, Z.
Milk as a Source of Camo
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/db_xref="taxon:9838"
/tissue_type="lactating mammary
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Bovidae; Bos.

1 chases 1 to 688)

Tydell, C.C., Yount, N., Tran, D., Yuan, J. and Selsted, M.E.
Isolation, characterization, and antimicrobial properties of boving oligosaccharide-binding protein. A microbicidal granule protein of
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/protein_id="AAL87002.1"
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/db_xref="taxon:9913"
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                                  AspProAlaCysCysSerProIleValProArgAsnGluTrpLysAlaLeuAlaSerGlu 40
                                                                                                                                                 MetLeuLeuAlaTrpAlaLeuProSerLeuLeuArgLeuGlyAlaAlaGlnGluThrGlu
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2 (bases 1 to 669)
Slayton, W.B., Rigaa, A., Hancock, J.D., Zaugg, J.K., Le, T.V.,
Trautman, M.S., Spangrude, G.J., Carroll, W.L. and Schibler, K.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Slayton, W.B., Rigaa, A., Hancock, J.D., Zaugg, J.K., Le, T.V., Trautman, M.S., Spangrude, G.J., Carroll, W.L. and Schibler, K.R. Granulocyte-colony stimulating factor up-regulates expression murine tag? during myeloid differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (11-OCT-1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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212 c 173 g 140 t
                                                                               -TGCAGTTTCATCGTGCCCCGCAGTGAGTGGAGGGCCCTGCCATCCGAG
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/cell_line="32D cl3"
                                                                                                                                                                                                                                                                                                                                                                  /product="TAG7-like protein"
/protein_id="AAF06335.1"
/db_xref="GI:6273361"
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Kang, D., Liu, G., Lundstrom, A., Gelius, E. and Steiner, H. A peptidoglycan recognition protein in innate immunity co from insects to humans

Proc. Natl. Acad. Sci. U.S.A. 95 (17), 10078-10082 (1998) 98374338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-JUL-1998) Microbiology, Stockholm S-106 91, Sweden
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Direct Submission
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                                                                                                             /codon_start=1
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                                                                /gene="Pgrp"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                      GTCATCCAAAGCTGGGAACACTACCGA 578
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IMAGE:3969014,
BC005582
BC005582.1 GI:
      USA
NIH-MGC
             Direct Submission
Direct Submission
Submitted (02-APR-2001) National Institutes of Health, Mammalian Submitted (02-APR-2001) National Institutes of Health, Mammalian Submitted (05-APR-2001) National Institutes of Health, Mammalian Submitted (MGC), Cancer Genomics Office, National Cancer Fratitute. 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                  Mus musculus Eukeazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 713)
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Mus musci
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                                                                                                                                                              house mouse
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 Project URL: http://mgc.nci.nih.
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             LysThrLeuGlyTrpCysAspValGlyTyrAsnPheLeuIleGlyGluAspGlyLeuVal 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: MGC help desk
Email: cyapbs r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site:
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DHTGPTWNPMSIGITEMGHENRVPAKRALRAALNLLECGVSRGFLRSNYEVKGHRDV
QSTLSPGDQLYQVIQSWEHYRE"
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/protein_id="AAH05582.1'
/db_xref="GI:13542756"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="MGC:11430 IMAGE:3969014"
/tissue_type="Mammary tumor. Met.
model. 10 month old virgin mouse
/clone_1lb="NCI_CGAP_Mam1"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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S., Martin, R.G.,
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Hale, Hale, S.M., Muzny, D.M.,

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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                             Submitted (25-MAY-1999)
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Mammalia; Eutheria; Rodentia;
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VQSTLSPGDQLYEIQSWDHYNE"
193 c 166 g 137 t
                                                                                                                                                                                                                        /note="similar to Homo sapiens and Mus musculus peptidoglycan recognition protein; similar to T. nand Mus musculus TAG7"
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20. .571
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                                                                                                                                                                                                                                                /note-"similar
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Submitted (18-APR-1995) O.S.
Submitted of Science,
     9660837
On Jul (
                                                                             Kiselev,S.L., Kustikova,O.S., Korobko,E.V.,
Kabishev,A.A., Lukanidin,E.M. and Georgiev,
Molecular cloning and characterization of t
                                                                                                                                                                                                                                                                                      Kustikova,O.S., Kiselev,S.L., Borodulina,O.R., Afanas'eva,A.V. and Kabishev,A.A. Cloning of the tag7 gene expressed in metastati Genetika 32 (5), 621-628 (1996)
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/protein_id=Ca60133.1"
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/db_xref="MGD:MGI:107415"
/db_xref="MGD:MGI:107415"
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DHTGFTWNPMSIGTFYGNFWDRVRKAGPPCCPKSSGIWGVSGLPEIQL"
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/db_xref="taxon:10090"
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/dev_stage="adult"
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Burkhart-Schultz,K., Gordon,L., Scott,D., Johnson,G., Stilwagen,S., Phan,H., Velasco,N., Do,L., Regala,W., Terry,A., Danganan,L., Erler,A., Christensen,M., Georgescu,A., Avila,J., Attix,C., Andreise,T., Amico-Keller,G., Coefield,J., Duarte,S., Lucas,S., Bruce,R., Thomas,P., Quan,G., Kronmiller,B., Arellano,A., Sanders,C., Ow,D., Nolan,M., Trong,S., Kobayashi,A., Olsen,A.S. and Carrano,A.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (11-JUN-1999) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from q centromere to telomere. BAC 282485 overlaps cosmid R30477 to the left from bases 1 to 4,419 of this accession, and overlaps BAC 264576 (CIT-B-297N14; AC006262) from
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complement(472..712)
/rpt_family="AluJb"
/note-"Hypothetical arginine-rich gene product;
Hypothetical CDS constructed from overlapping ESTs and
Hypothetical CDS constructed from overlapping ESTs and
Xgrail predictions. EST coverage is lacking for some
portions of the CDS. Gene may be alternatively spliced, as
multiple transcripts map into this region; alternatively,
these individual clones may represent artifactual events
during RT and cDNA creation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(472. .712)
/rpt_family="MIR"
/rpt_family="MIR"
join(<746. .904,1157. .1239,4294. .4451,5875. .6036,
12784. .12994,13080. .13162,13903. .13958,14053. .14128,
1429. .14568,14726. .14804,14982. .15039,15813. .15885,
                                                                                                                                                                                                                          /evidence=not_experimental
/product="BC282485 1"
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/clone="CIT-B-344H19"
/clone_lib="Cal Tech CIT-B BAC library"
/note="LLNL clone name: BC282485"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                             /codon_start=3
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SELALYKRGGRGSRGRGRPARPSPSPTGGRALRFDPTAFVKAKERKQREIQMKQQQRN RLGSGGSGDGPSVSWSRQTQPPAALTGRGDAPNRSRNRSSSVDSFRSRCSSASSCSDL EDFSESLSRGGHRRRGKPPSPTPWSGSNMKSPPVERSHHQKSLANSGGWVPIKEYSSE

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misc_feature
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/note="DDS similarity to overlapping ESTs:
/note="DDS similarity to overlapping ESTs:
N39722 yx92e04.rl Homo sapiens CDNA clone 269214 5';
(256...43B); 81$ identity.-AA283147 zt14d07.rl
NCI_CGAP_GCB1 Homo sapiens cDNA
clone IMAGE:713101 5'; (248...400); 99$ identity.-AA143160
z149d07.rl Soares pregnant uterus NDHPU Homo sapiens cDNA
clone 505261 5'; (127...281); 97$ identity.-N28707
yx66d11.rl Homo sapiens cDNA clone 266709 5'; (67...222);
98$ identity.-AA142881 z149407.sl Soares pregnant uterus
NDHPU Homo sapiens cDNA clone 505261 3'; (437...275); 97$
tabnetity."
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/note="DDS similarity to overlapping ESTs:
/note="DDS similarity to overlapping ESTs:
/N39722 yys2064 rl Homo sapiens cDNA clone 269214 5';
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pregnant uterus NDHPU Homo sapiens cDNA clone 505261 5';
/282. 379); 100% identity.-AA142881 zl49d07.sl Soares
pregnant uterus NDHPU Homo sapiens cDNA clone 505261 3';
/274. 175); 95% identity."
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N39722 yx92e04.rl Homo sapiens cDNA clone 269214 5';
N39722 yx92e04.rl Homo sapiens cDNA clone 269214 5';
(12. 170); 99% identity.-AA283147 ztl4d07.rl NCI_CGAP_GCB1
Homo sapiens cDNA clone IMAGE:713101 5'; (6. .163); 99%
identity.-AA143160 z149d07.rl Soares pregnant uterus NDHPU
HOmo sapiens cDNA clone 505261 5'; (1. .43); 100%
identity.-AA142881 z149d07.sl Soares pregnant uterus NDHPU
Homo sapiens cDNA clone 505261 3'; (570. .527); 64%
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/rpt_family="LINE2"
complement(2200..2498)
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N39722 yx92e04.rl Homo sapiens cDNA clone 269214 5';
(171. .255); 95% identity.-AA283147 zt14d07.rl
NCI_CGAP_GCB1 Homo sapiens cDNA
clone IMAGE:713101 5'; (164. .247); 92% identity.-AA143160
z149d07.rl Soares pregnant uterus NbHPU Homo sapiens cDNA
clone 505261 5'; (44. .126); 100% identity.-N28707
yx66d11.rl Homo sapiens cDNA clone 266709 5'; (1. .66); 98%
identity.-AA142881 z149d07.sl Soares pregnant uterus NbHPU
Homo sapiens cDNA clone 505261 3'; (526. .438); 82%
  /rpt_family="AluSx"
complement(6608. .6648)
/rpt_family="LINE2"
                                                                  /note="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 100.000"
complement(6148. .6443)
                                                                                                                                    /note-"DDS similarity to N28707 yx66dl1.rl Homo sapiens cDNA clone 266709 5'; (223. .246); 100% identity." 5906. .6036
                                                                                                                                                                                                                                                                                                                                                                                complement(4789. .5083)
/rpt_family="AluSx"
5875. .5972
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/rpt_family="Alusx"
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complement(1673. .19
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complement(2576
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complement/occo
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complement(11914. .11976)
/rpt_family="AT_rich"
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/rpt_family="MIR"
complement(7538. .7639)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="predicted exon, program: grail2exons_human_1.3, frame: 2, quality: excellent, score: 100.000-DDS similarity to AA765166 nz79c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1301672; (122. .48); 100%
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/rpt_family="LIM1"
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complement(12107
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11775. .11814
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/rpt_family="AluJ"
11322..11619
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/rpt_family="GC_rich"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12895. .12994
/note="DDS similarity to AA765166 nz79c05.sl NCI_CGAP_GCB1
Homo sapiens cDNA clone IMAGE:1301672; (222. .123); 97%
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frame: 1, quality: excellent, score: 92.000"
12847. .12908
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complement/????
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/rpt_family="AluJ"
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Matches:
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17264 ATGGGTGAGTGACTGTCCAGCCAGTTGGGATGGGGGCCTGACACGGGGCCCTACGCTATCA 17205
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(PGLYRPIalpha)
AY035376
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Mammalia; Eutheria;
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TWPHFKH"
                                                                                                                                                            /product="peptidoglycan recognition
precursor"
                                                                                                                                                                                                                   cytoplasmic domain"
                                                                                                                                                                                                                               immunity pattern recognition molecule; contains transmembrane domains, 2 extracellular domains,
                                                                                                                                                                                                                                                                                                                       /gene="PGLYRPIalpha"
/note="PGRPIalpha"
                                                                                                                                                                                                                                                                  /gene="PGLYRPIalpha"
/note="PGRP-I-alpha; member of PGRP family; innate
                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                             /protein_id="AAK72484.1"
                                                                                                                                                                                               codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="]
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgGlyTrpAsnPheThrGlyAlaHisSerGlyHisLeuTrpAsnProMetSerIleGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyTrpCysAspValGlyTyrAsnPheLeuIleGlyGluAspGlyLeuValTyrGluGly 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---ATGAACCTCCCAGCCAAATATGTCATCATCATCCACACCGCTGGCACAAGCTGCACT
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                                                                                                                                                                                                                            GlyHisArgAspValGlnArgThrLeuSerProGlyAsnGlnLeuTyrHisLeuIleGln 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTATCCACAGACTGCCAGACTGTCGTCCGAAACATACAGTCCTTTCACATGGACACACGG
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                                                                                                                         ACCTGGCCTCATTTCAAG
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                                                                                                                                                                                               GGCCACAGTGACGTCGACATCCTGTCCCCTGGGCAGGCTTTGTATAACATCATCAGC
                                                                                                                                                                                                                                                                CAGGACCTGATCCAGTGTGCCGTGGTTGAGGGGTACCTGACTCCAAACTACCTGCTGATG
                                                                                                                                                                                                                                                                                                                                                                      IleSerPheMetGlyAsnTyrMetAspArgValProThrProGlnAlaIleArgAlaAla 143
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BACR21H10;
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/note="Region: conserved
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44D2-44E1, BAC clone
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REFERENCE AUTHORS TITLE

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Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,
Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Woshrefi, A.,
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J.,
Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B.,
Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Syirskas, R., Tector, C., Williams, S.M.,
Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
Sequencing of Drosophila chromosome 2R, region 44D2-44E1
   IleValProArgAsnGluTrpLysAlaLeuAlaSerGluCysAlaGlnHisLeuSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Cicsiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawrence Berkeley National Laboratory, MS 64-121 Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-MAR-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Mar 17, 2001 this sequence version replaced gi:5670628. Sequence submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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|strain-"y; cn bw sp"
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                                                                                                           2 (bases 1 to 169509)

Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.

Butenhoff, C., Champe, M., Chavez, C., Chew, M., Clesiolka, L.,

Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,

Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,
                                                                                                                                                                                                                                                                                             Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C., Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A., Carlson,J.W., Center,A., Champe,M., Dyle,C., Dresnek,D., Farfan,D., Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D., Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J., Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J., Parello,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B., Phouanenavong,S., Pittman,G.S., Purl,V., Richards,S., Scheeler,F., Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M., Sequencing of Drosophila chromosome 2R, region 44E-44F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster, chromosome BACR43I04, complete sequence.
Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Packb,J.K., Park,
Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.
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1 (bases 1 to 169509)
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JOURNAL
                                                                                                                                    105562 TCCGATGCGGTCAGTCGCGGCCAGATCGTTTCCGGATACATCCTGTACGGACATCGGCAG
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105442
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TGGAAGGCC
                                  TyrArgSer 190
                                                                 GTCGGCTCCACCGAGTGCCCCGGCACCAACATCTGGAACGAGATCCGCACCTGGTCCAAC 105443
                                                                                                 ValGlnArgThrLeuSerProGlyAsnGlnLeuTyrHisLeuIleGlnAsnTrpProHis
                                                                                                                                                                                                                                         GlyAsnTyrMetAspArgValProThrProGlnAlaIleArgAlaAlaGlnGlyLeuLeu 147
                                                                                                                                                                                                                                                                               GTTATGGGTGCTCACGCCACTAAC--
                                                                                                                                                                                                                                                                                                     PheThrGlyAlaHisSerGlyHisLeuTrpAsnProMetSerIleGlyIleSerPheMet 127
                                                                                                                                                                                                                                                                                                                                                                                                                   TGCATCACACAGCTGCAGAACATCCAGGCCTACCACATGGACTCCCTGGGCTGGGCCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (14-APR-1999) Drosophila Genome Center, Lawrence Laboratory, MS 64-121, Berkeley, CA 94720, USA On Apr 21, 2001 this sequence version replaced gi:6435866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawrence Berkeley National Laboratory, MS 64-121 Berkeley, CA 94720
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105434
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/strain="y; cn bw sp"
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Direct Submission
Submitted (30-DEC-1999) Celera Genomics, 45 West
Rockville, MD, USA
This sequence was identified as CDM:10213218 by
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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SIGNAL 1 21
CHAIN 22 196
DISULFID 67 73
CARBOHYD 112 112
SEQUENCE 196 AA; 21731 MP
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                                                        Trautman M.S., Kigaa A., Hancock J.D., Zaugg J.K., Le T.V., "Granutman M.S., Spangrude G.J., Carroll W.L., Schibler K.R.; "Granutocyte-colony stimulating factor up-regulates express: murine tag7 during myeloid differentiation."; Submitted (OCT-1999) to the EMBL/Gamanaria
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EMBL;
HSSP;
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Small intestine;
MEDLINE-21085660; PubMed-11217851;
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MEDLINE-98374308; PubMed-9707603;
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Kabishev A.A., Lukanidin E.M., Georgie
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., FUNCTION, AND MEDLINE-98325081; PubMed-9660837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptidoglycan recognition PGLYRP OR PGRP OR TAG7.
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AF242517; AAF9
P00806; 1ARO.
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AAF99598
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Rodentia;
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POTENTIAL.
N-LINEED (GLCNAC. . .) (POTENTIAL);
D954C51440DC27DC CRC64;
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Sciurognathi;
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Pred. No. 5
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                                                                                                                                                                                                                                                          G.P.;
of the mouse tag7
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SIGNAL
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                                                                                                                                                                                                                                                                     EMBL;
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Immune response; Cytokine;
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Submitted (APR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
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    113
                       121
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                                                                                                   1 MILAWALPSILRIGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHTAGS 60
                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: EXISTS IN BOTH SOLUBLE AND MEMBRANE-ASSOCIATED FORMS.

TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SPLEEN AND LUNG. ALD TISCTED IN BRAIN AND THYMUS. IN THE LUNG, EXPRESSED IN THE DITECTED IN BRAIN AND IN CHERTAIN, EXPRESSED IN THE PURKINJE OF THE CEREBELLUM AND IN CERTAIN LAYERS OF NEURONS IN THE HIPPOCAMPUS. ALSO DETECTED IN CELLS FILLING THE SPACE WITHIN INTESTINAL VILLUS.

SIMILARITY: BELONGS TO THE PEPTIDOGLYCAN RECOGNITION PROTEIN
                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitted (APR-2001) to the EMBL/GenBank/DDBJ databases. FUNCTION: BINDS SPECIFICALLY TO PEPTIDOGLYCAN AND IS INNATE IMMUNITY. THE SOLUBLE FORM TRIGGERS APOPTOSIS SUBCELLULAR LOCATION: EXISTS IN BOTH SOLUBLE AND MEMB
           SIGISEMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYH
                                         SIGITFMGNFMDRVPAKRALRAALNLLECGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQ
                                                                                   AF076482;
AF193843;
AK008335;
BC005582;
                                                                                                                                                                                                                                     X86374; CAA60133.1;
Y12088; CAA72803.1;
                                                                                                                                                                                                                                                                                                             non-profit institutions as long as its content is d and this statement is not removed. Usage by and for srequires a license agreement (See http://www.isb-sib.an email to license@isb-sib.ch).
                                                                                                                                         Similarity
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182
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                                                                                                                                Conservative
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182
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                                                                                                                                       65.8%; Score 67.2%; Pred.
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                                                                                                                                                                        WW;
                                                                                                                                                                                 Apoptosis; Signal.
POTENTIAL.
PEPTIDOGLYCAN RECOGNITION PROTEIN.
POTENTIAL.
                                                                                                                                21;
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., Yamanaka
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16-OCT-2001
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed
entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A peptidoglycan recognition protein in innate imm insects to humans:", Proc. Natl. Acad. Sci. U.S.A. 95:10078-10082(1998)-1- FUNCTION: BINDS SPECIFICALLY TO PEPTIDOGLYCAN PROPENCLOXIDASE CASCADE WHICH IS AN IMPORTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; (Ditrysia; Noctuoidea; Noctuidae; Plusiinae; Trichoplusia.
                                                                                                                                                                                                                                                          EMBL; AF076481; AAC31820.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Larva;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76537;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation updat
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SUBUNIT: MONOMER (PROBABLE).

TISSUE SPECIFICITY: STRONGLY EXPRESSED IN

TISSUE SPECIFICITY: IN HEMOCYTE, NO EXPRES
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           ACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHLIQNWPHY 188
                                                       VGYNFLIGEDGLYYEGRGWNFTGAHSGHLWNPMSIGISFMGNYMDRVPTPQAIRAAQGLL 147
                                                                                        VVTKDEWDGLTPIHVEYLARPVELVIIQHTVTSTCNTDAACAQIVRNIQSYHMDNLNYWD
                                           IGSSFIIGGNGKVYEGAGWLHVGAHT-YGYNRKSIGITFIGNYNNDKPTQKSLDALRALL
                                                                                                             IVPRNEWKALASECAQHLSLPLRYVVVSHTAGSSCNTPASCQQQARNVQHYHMKTLGWCD
                                                                                                                                                                                                                                                 response;
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                                                                                                                                                    Similarity
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                                                                                                                                                                                       182
                                                                                                                                                                                                                                                                                 equires a license agreement (See http://www.lsb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                        Conservative
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                                                                                                                                                                                       AA;
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                                                                                                                                                                                                                                              Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMeu-Lundstroem A., Gea-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=9707603;
                                                                                                                                                                                                              16
182
140
                                                                                                                                                  37.0%;
                                                                                                                                                                                    20572 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                        35;
                                                                                                                                       Score 388.5;
Pred. No. 2.3e
95; Mismatches
                                                                                                                                                                                    POTENTIAL.
; 56631E762AE34794 CRC64;
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                                                                                                                                                                                                                        PEPTIDOGLYCAN RECOGNITION PROTEIN
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                                                                                                                                                                                                                                                                                                                                                    a collaboration
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Best Local S
Matches 72
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Hemolymph;
MEDLINE-96278824; PubMed-8662762;
Yoshida H., Kinoshita K., Ashida
"Purification of a peptidoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., SEQUENCE OF 24-72; TISSUE SPECIFICITY, AND INDUCTION. STRAIN-Kinshu X Showa; TISSUE-Fat body; MEDLINE-99223509; PubMed-10207004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Mandibulata; Insecta; Pterygota; Neoptera; Endopterygota; Ditrysia; Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 24-43,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ochiai M., Ashida M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGRP_BOMMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immune response; Signal.
                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: MONOMER (PROBABLE).
TISSUE SPECIFICITY: CONSTITUTIVELY
EPITHELIAL CELLS AND HEMOCYTES. NO
TUBULES, SILK GLAND OR MIDGUT.
INDUCTION: BY BACTERIAL CHALLENGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE PEPTIDOGLYCAN RECOGNITION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene of the silkworm, Bombyx mori
3iol Chem. 274:11854-11858(1999).
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SIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYH
                                                                                                                                                                                                                                                                                       MILIAWALPSILIRIGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHTAGS
                                                                                              FCRTDAGCEELVRNIQINHMEALQYWDIGPSFLVGGNGKVYEGSGWLHVGAHT-YGYNSR
                                                                                                                                      SCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNPM
                                                                                                                                                                                                                          VVLALALSSLL-----TEIAADCD-VVSKKQWDGLIPVHVSYLARPVSLVIVQHTVTP
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AB016249; BAA77209.1;
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61
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147
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                                                                                                                                                                                                                                                                                                                                                       Score 345.5; DB 1
Pred. No. 3.4e-26;
6; Mismatches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDOGLYCAN RECOGNITION PROTEIN POTENTIAL. POTENTIAL.
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Lepidoptera;
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Glossata;
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                                                       Query Match
Best Local :
                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                   Beck P.J., Gonzalez S., Ward C.L., Molineux I.J.;

"Sequence of bacteriophage T3 DNA from gene 2.5 through gene 9.";

J. Mol. Biol. 210:687-701(1989).

"I FUNCTION: THIS PROTEIN IS NOT REQUIRED FOR LYSIS BUT PLAYS AN IMPORTANT ROLE IN DNA SYNTHESIS. IT IS KNOWN TO DETACH THE HOST CHROMOSOME FROM THE BACTERIAL MEMBRANE TO WHICH IT IS NORMALLY BOUND. IT IS A BIFUNCTIONAL PROTEIN THAT CUTS AMIDE BONDS IN THE BACTERIAL CELL WALL AND BINDS TO AND INHIBITS TRANSCRIPTION BY

T3 RNA POLYMERASE (BY SIMILARITY).

T4 RNA POLYMERASE (BY SIMILARITY).
                                                                                                 METAL
                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is proceed the EMBL our the Swiss Institute of Bioinformatics and the EMBL our three are no restrictions is in
                                                                                      SEQUENCE
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                                                                                                                                                               INIT_MET
                                                                                                                                                                         Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, T7-like viruses.
                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage T3.
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16-OCT-2001
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    30
                      73
                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS, TO THE N-ACETYLMURAMOYL-L-ALANINE AMIDASE
                                                                                                                                                                                                                                                                                                                                                                                       91ycopeptides.
COFACTOR: ZINC (REQUIRED ONLY FOR AMIDASE ACTIVITY)
                                                                                                                                                                                                                                                                                                                                                                     ENZYME REGULATION: BINDING
ACTIVITY (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                residues and L-amino acid
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                                                                                                                                                                                  PF01510; Amidase_2;
                                                                                                                                                                                                         P00806; 1ARO
                                                                                                                                                                                                                              X17255; CAA35133.1; -.
                                            36;
                                                       Similarity
                                                                                                                                                                                                                                               an email to license@isb-sib.ch).
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                                            Conservative
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130
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46
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                                           18;
                                                                                             ZINC (BY SIMILARITY).
ZINC (TO THE HYDROXYL GROU
THROUGH A WATER MOLECULE)
SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA stage; Caudovirales;
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annotation updat
                                          Score 127; DB Pred. No. 2.5e.8; Mismatches
                                                                                                                                                              BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                     RNA POLYMERASE
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                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                               in
                                                    DB 1;
.5e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                               certain bacterial
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                                                              Length 150
                                                                                    CRC64;
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                                          Indels
                                                                                                                                        GROUP
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                                                                                                                                                                                                                                                                                                                                                                    INHIBITS AMIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Podoviridae;
                                                                                                                             (BY
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                                                                                                                                        OF.
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                                                                                                                                        TYR
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                                         Gaps
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95099869; PubMed-7801634;
Huang W., Cui X., Tian Y., Lin M., Peng X.;
"Cloning of T7 lysozyme gene and construction of the vector
transgenic plants resistant to bacterial infection.";
Wei Sheng Wu Hsueh Pao 34:261-265(1994).
                                                                                                                                             -
                                                                                                                                                                                                                           EMBO
                                                                                                                                                                                                                                          Jeruzalmi D., Steitz T.A.;
"Structure of T7 RNA polymerase
inhibitor T7 lvsozvme ":
                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.8 MEDLINE=98336199; PubMed=96
                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND MEDLINE=94224877; PubMed=8171031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
01-FEB-1995 (Rel. 31, Last sequence up
16-CCT-2001 (Rel. 40, Last annotation
N-acetylmuramoy1-L-alanine amidase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete nucleotide sequence of bacteriophage T7 locations of T7 genetic elements.";
J. Mol. Biol. 166:477-535(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-83241725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T7-like viruses.
NCBI_TaxID-10760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P00806; Q38567;
21-JUL-1986 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAAA_BPT7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Nucleotide sequence from the genetic left end of bacteriophage NA to the beginning of gene 4.";
J. Mol. Biol. 148:303-330(1981).
                                                                                                                                                                                                                                      nhibitor T7
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e European Bloirf
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                                                                                                                        T7 RNA POLYMERASE.
CATALYTIC ACTIVITY: Hydrolyzes the CATALYTIC and L-amino acid residues
                                                                                                                                                            FUNCTION: THIS PROTEIN IS NOT REQUIRED FOR LYSIS BUT PLAYS AN INFORMATION FOLD IN DAS SYNTHESIS. IT IS KNOWN TO DETACH THE HOST CHROMOSOME FROM THE BACTERIAL MEMBRANE TO WHICH IT IS NORWALLY BOUND. IT IS A BIFUNCTIONAL PROTEIN THAT CUTS AMIDE BONDS IN THE BACTERIAL CELL WALL AND BINDS TO AND INHIBITS TRANSCRIPTION BY
                                                                      ACTIVITY.
SIMILARITY:
                                                                                             ENZYME REGULATION:
                                                                                                          glycopeptides.
COFACTOR: ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.J., Studier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.J., Studier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVP-----TPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQL
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                                                                                                                                                                                                                           or T7 lysozyme.";
17:4101-4113(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dsDNA viruses,
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                                                                      BELONGS
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                                                                                                                                                                                                                                                                       Pubmed=9670025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=7310871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=6864790;
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                                                                     THE N-ACETYLMURAMOYL-L-ALANINE
                                                                                                                                                                                                                                                                                                        91:4034-4038(1994)
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                       ght. It is produced through Bioinformatics and the EM
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lysozyme, a
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                                                                                            INHIBITS
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Matches 37
       P95442;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update
Hydroxydechloroatrazine ethylaminohydrolase
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EMBL; V01127; CAA22346.1; --
EMBL; S75616; AAB32819.1; --
PIR; A01001; MUBPA7.
PIR; S42302; S42302.
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     Hydroxyatrazine
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                                                                                                            RNVQHYHMKTLGWCDVGYNFLIGEDGLVYBGRGWNFTGAHSGHLWNPMSIGISFMGNYMD
                                                                            KGKFDANFTPAQMQSLRSLLVTLLAKYEGA-----VLRAHHEVAPKACPSFDL
                                                                                          RVP----
                                                                                                     REIROWH-KEOGWLDVGYHFIIKRDGTVEAGRDEMAVGSHAKG-YNHNSIGVCLVGGIDD
                                                                                                                                                                                                                                                                                                                                                                                                                  1LBA; 30-APR-94.
1ARO; 21-OCT-98.
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                                                                                                                                        Similarity
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                                                                                       -TPQAIRAAQGLLACGVA--QGALRSNYVLKGHRDVQRTLSPGNQL
                                                                                                                                                           Ä,
                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                              protein;
     hydrolase).
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                                                                                                                                      12.1%;
                                                                                                                                                                                                                                                                                                                                                                                              Zinc;
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Pred. No. 2.5e
19; Mismatches
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ZINC (TC
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V -> G (
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                 update)
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                                                                                                                                      DB 1;
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           (EC 3.5.99.3)
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                              SURE_HELPJ
Q9ZKSO;
30-MAY-2000
30-MAY-2000
15-JUN-2002
                           Gibson A.
                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Acid phosphatase surE (EC 3.1.3.2).
SURE OR JHP0865.
                                          SEQUENCE FROM N.A.
MEDLINE-99120557; PubMed-9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King
Smith D.R., Noonan B., Guild B.C., deJon
Tummino P.J., Caruso A., Uria-Nickelsen
Gibson R., Merberg D., Mills S.D., Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U66917; AAC45138.1; -.
InterPro; IPR002604; ATZ_TRZ
Pfam; PF01685; ATZ_TRZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as lon-
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                      NCBI_TaxID-85963;
                                                                                                                                                                                                                                                                    Helicobacter pylori J99 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enzyme of a novel atrazine degradation pathwappl. Environ. Microbiol. 63:916-923(1997).
-i- FUNCTION: TRANSFORMS HYDROXYATRAZINE TO (DIHYDROXY-ISOPROPYL-ATRAZINE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The atzB gene of Pseudomonas sp. strain ADP encodes enzyme of a novel atrazine degradation pathway.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boundy-Mills K.L.,
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MEDLINE-97208208; PubMed-9055410;
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Bacteria; Prot
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CATALYTIC ACTIVITY: 4-(ethylamino)-2-hydroxy-6-(isopropylamino)-
1,3,5-triazine + H(2)0 = N-isopropylammelide + ethylamine.
PATHWAY: Atrazine degradation-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: BELONGS TO THE ATZ/TRZ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDIPAMAAAGVRVGFGVDGH
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  sequence comparison
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                                                                                                                                                                                                                                                         (Campylobacter pylori J99).
a; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333
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two unrelated isolates
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                                        King B.L., Brown E.D., Doi
deJonge B.L., Carmel G.,
elsen M., Mills D.M., Ives
Jiang Q., Taylor D.E., Vov
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TIGREAMS; TIGR00087; SurE; 1
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Pfam; PF01975; SurE;
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#WAY-2000 (Rel. 39, Last sequence up
TUN-2002 (Rel. 41, Last annotation
phosphatase surE (EC 3.1.3.2).
OR HP0930.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Cytoplasmic (Potential).
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P42591;
01-NOV-1995
01-NOV-1995
16-OCT-2001
                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655;
STRAIN-KI2 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, B
Riley M., Collado-Vides J., Glasn
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                                                                                                                               Gregor J., Davis N.W.,
Mau B., Shao Y.;
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Nature 388:539-547(1997).
-!- CATALYTIC ACTIVITY: An
                                                               "The complete genome sequence Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: BELONGS TO THE SURE ACID PHOSPHATASE FAMILY.
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Submitted (FEB-1998) to the EMBL/GenBank/DDB
-I- SUBCELLULAR LOCATION: Secreted.
-I- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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                                                                                           EMBL; AF046870; AAC03101.1; HSSP; P00736; 1APQ.
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EGF-containing fibulin-like extracellular
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RESULT 12
VS41_GTAL
ID VS41_G
AC P92127
DT 16-OCT
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Eukary
OX NCBI_T
RN [1]
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RX MEDLIN
RA Papana
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Best Local S
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SMART; SM000179; EGF_CA; 4.

SMART; SM00001; EGF_like; 2.

PROSITE; PS00010; ASX_HYDROXYL; 4.

PROSITE; PS00022; EGF_1; FALSE_NEG.

PROSITE; PS01187; EGF_CA; 6.
                                                                               STRAIN-02-4A1;

MEDLINE-97321554; PubMed-9178264;

Papanastasiou P., Bruderer T., Li Y., Bor

"Primary structure and biochemical proper

surface protein of Giardia.";

Mol. Biochem. Parasitol. 86:13-27(1997).
                                                                                                                                                                                                                                                                                                                                VS41_GIALA
P92127;
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CARBOHYD
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CHARACTERIZATION.
CHARACTERIZATION.
MEDLINE-97233006; PubMed-9078242;
Papanastasiou P., McConville M.J., Ralton
"The variant-specific surface protein of G
                                                                                                                                                                                                                              16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Variant-specific surface protein VSP4A1 precursor
Giardia lamblia (Giardia intestinalis).
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
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DOMAIN
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16-OCT-2001
                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                             (Rel. 40, Created)
(Rel. 40, Last sequence up
(Rel. 40, Last annotation
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242
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EGG-LIKE 1, DIVERGENT.

EGG-LIKE 2, CALCIUM-BINDING (POTENTIA)

EGG-LIKE 3, CALCIUM-BINDING (POTENTIA)

EGG-LIKE 4, CALCIUM-BINDING (POTENTIA)

EGG-LIKE 5, CALCIUM-BINDING (POTENTIA)

EGG-LIKE 6, CALCIUM-BINDING (POTENTIA)

EGG-LIKE 7, CALCIUM-BINDING (POTENTIA)

EGG-LIKE 6, CALCIUM-BINDING (POTENTIA)

EGG-LIKE 7, CALCIUM-BINDING (POTENTIA)

EGG-LIKE 8, CALCIUM-BINDING (POTENTIA)

EGG-LIKE 1, CALCIUM-BINDING (POTENTIA)

EGG-LIKE 1, CALCIUM-BINDING (POTENTIA)

EGG-LIKE 1, CALCIUM-BINDING (POTENTIAL)

EGG-LIKE 1, CALCIUM-BINDING (POTENTIAL)

EGG-LIKE 1, CALCIUM-BINDING (POTENTIAL)

EGG-LIKE 1, CALCIUM-BINDING (POTENTIAL)

EGG-LIKE 2, CALCIUM-BINDING (POTENTIAL)

EGG-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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Pred. No. 7.4;
11; Mismatches
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                                                                                                                Y., Bommeli
I properties
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   n J., Koel
Giardia,
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                  Koehler
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   vsp4A1,
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                                                                                                                                  Koehler
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                                                                                                                   variant-specific
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(POTENTIAL).
(POTENTIAL).
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Best Local Similarity
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01-OCT-1996
15-JUN-2002
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                                                                                                                                                     STRAU
                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
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                                           Streptomyces aureofaciens. Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000561; EGF-like.
InterPro; IPR002174; Furin-like.
InterPro; IPR005127; Giardia_VSP.
Pfam; PF03302; VSP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycosylated
Biochem. J.
                                                                           enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
   SEQUENCE
                      NCBI_TaxID-1894;
                                Actinomycetales;
                                                                                    1,4-alpha-glucan
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART;
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                                                                                                                                                                                                                                                                                                                                            GAAQETEDPA----C--CSPIVPRNEWKALASECAQHLSLPLRYVVVSHTAGSSCNTPAS
                                                                                                                                          STRAU
                                                                                                                                                                                              GNPLGTIAGGNAYVGVEGCSQCTAP
                                                                                                                                                                                                                   GVAQGALRSNYVLKGHRDVQRTLSP
                                                                                                                                                                                                                                      SYCAAGFFLYMGGCYKIDTVPGSYMCSKSTTAGVCDTPNANNRFFVVPKAISAEQSVLAC
                                                                                                                                                                                                                                                            NPMSIG-ISFMGN--YMDRVP-----
                                                                                                                                                                                                                                                                                CGGTSGACDAIVIDANGKEHYY---CSYCGETNKFPI--DGLCTDNKGTN--AGCTDHTC
                                                                                                                                                                                                                                                                                                      CQQ----
                                                                                                                                                                                                                                                                                                                           GCAECTKEPAGPLKCTKCKP---
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O14763; 1D0G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00181;
SM00001;
SM00261;
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  FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                          682
687
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(Rel. 41, Last annotation
lucan branching enzyme (EC
                                                                                                                     (Rel.
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:; Transmembrane;
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EGF_like; 1.
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:49-56(1997).
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                                Streptomycineae;
                                                                                                                                                                                                                                                                                                    -QARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLW
                                                                                                                                                                                                                                                                                                                                                                           7.1%;
22.4%;
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                                Actinobacteria (class); Actinobacteridae; ycineae; Streptomycetaceae; Streptomyces.
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Pred. No.
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D892F675D626D7EC CRC64;
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EXTRACELLULAR (PC
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                                                                                                                                          PRT;
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2.4.1.18) (Glycogen
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RESULT
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30-MAY-2000 (Rel. 39, Last s
15-JUN-2002 (Rel. 41, Last s
Murc/ddl bifunctional enzymu
ligase (EC 6.3.2.8) (UDP-N-r
alanine-D-alanine ligase (
(D-Ala-D-Ala ligase)).
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084767;
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ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                MEDLINE-99000809; PubMed-9784136; Stephens R.S., Kalman S., Lammel (Mitchell W.P., Olinger L., Tatuso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
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Biochim. Biophys. Acta 1200:334-336(1994).
-I- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic
                                                                Chlamydia trachomatis.";
Science 282:754-759(1998)
                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-D/UW-3/Cx;
                                                                                                                                                                                                                                                                                                  Chlamydia trachomatis. Bacteria; Chlamydiales;
                                                                                                                                                                                                                                                                                                                                               MURC/DDL OR CT762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ATCC 10762 / CCM 3239;
MEDLINE-94347823; PubMed-8068720;
                                                                                                                                  Davis R.W.;
                                                                                                                                                                                                                                                                            NCBI_TaxID=813;
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                                                                                                          Genome sequence of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90
FUNCTION: CELL WALL FORMATION.

CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl phosphate + UDP-N-acetylmuramoyl-L-alanine.
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glycogen biosynthesis; third step.
subunit: MONOMER (BY SIMILARITY).
similarity: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no with the state of the state o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YRFLPALGELDLHLIGEGRHEELWTALGSQPMEHQGVAGTRFTVWAPNALGVRVTGDFSY 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00128; alpha-amylase;
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440 440 BY SIMILARITY.
493 493 BY SIMILARITY.
561 561 BY SIMILARITY.
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IPR004193; Isoamylase_N.
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    Last sequence update)
    Last annotation update;
    Last annotation update;
    Includes: UDP-N-acetylmuramate--alanine
    (UDP-N-acetylmuramoy]-L-alanine synthetase);

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32.6%;
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R InterPro; IPR000713; Mur_ligase.
R InterPro; IPR0004101; Mur_ligase_C.
)R InterPro; IPR0004101; Mur_ligase_C.
)PR InterPro; IPR004101; Mur_ligase_C.
)PR Pfam; PF01820; Dala_Dala_ligas; 1.
DR Pfam; PF01820; Dala_Dala_ligas, 1.
DR Pfam; PF01820; Dala_Dala_ligase_C; 1.
DR TIGRPAMS; TIGR01205; D_ala_Dala_TIGR; 1.
DR PROSITE; PS00844; DALA_DALA_LIGASE_1; 1.
DR PROSITE; PS00844; DALA_DALA_LIGASE_1; FALSE_NEG.
DR PROSITE; PS00844; DALA_DALA_LIGASE_2; FALSE_NEG.
RROSITE; PS00844; DALA_DALA_LIGASE_C: FALSE_NEG.
END PROSITE; PS00844; DALA_DALA_LIGASE_C: FALSE_NEG.

WWW Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
KW ATP-binding; Multifunctional enzyme; Complete proteome.

KW ATP-binding; Multifunctional enzyme; Complete proteome.

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TSA4_GIALA
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Best Local
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or send a
                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ATCC 30957 / WB;
MEDLINE-90280395; Pubmed-2352929;
                                                                                                                                                                                                                                                                                                      Giardia lamblia (Giardia Eukaryota; Diplomonadida; MCBI_TaxID=5741;
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                                                                                                   "Isolation and expression Giardia lamblia.";
                                                                                                                                                     Gillin F.D., Hagblom P., Harwood J., McCaffery M., So M., Guiney D.G.;
                                                                                                                                                                                                                                                                                                                                                                                      Major surface-labeled TSA 417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P21849;
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STRAIN-AD-1;
                        SEQUENCE OF 480-620
                                                                             Proc.
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SUBCELLULAR LOCATION: Cytoplasmic (I
SIMILARITY: IN THE N-TERMINAL SECTIO
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SMART; SM00001; EGF_like; 1.
SMART; SM00261; FU; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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InterPro; IPR005127; Giardia_VSP
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AAGGNTYKGIADCAECSAP
                      SPGNQLYHLIQNWPHYRSP
                                              --SLCLSSDGDGVCTEAAPGYFAPVGAANTEQSVIACGDTTGV--
                                                                    PMSIGISFMGNYMDRVPTP-----
                                                                                          GPSKT--LCPQH-----SAGKCTQCGGNSFMYKDGCYSSGEGL-----PGH---
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Copyright (c) 1993 - 2002 Compugen Ltd.
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O8spp7 bos taurus
O99ln4 rattus norv
O961b9 homo sapien
O9v4x2 drosophila
O961b8 homo sapien
O9v3b7 drosophila
O95sq9 drosophila
O8wmf9 sus scrofa
O9vyx7 drosophila
O8wmf9 sus scrofa
O9vyx7 drosophila
O9vyx7 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                          Q8wsz1
                                                                               Q8t5q2
1 bombyx mori
2 drosophila
5 homo sapien
4 homo sapien
9 drosophila
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O9fza8 arabidopsis P79941 xenopus lae O62353 caenorhabdi O88812 mus musculu	Q9FZA8 P79941 062353 088812	110 113	879 642 268 281		85.5 82 80.5	444
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Qysyo drosophila Qgnk7 drosophila 08634 mycobacteri Qgnk5 drosophila Qgnk6 drosophila Qgkzk5 streptomyce Q8xmx3 clostridium	Q9GNK7 Q9GNK5 Q9GNK5 Q9GNK6 Q9GNK6 Q9KZK5	1155155	299 539 520 138 416 222	21.8 21.3 21.0 17.3 16.9	229.5 229.5 224 221 181.5 177.5	654321
نه به به ۲۰۰۱ م.م.	Q8SXQ7 Q9VSW0 Q9VGN3 Q9QXZ1 Q9VV96 Q9VSV9	, v v T v v v	369 337 215 500 182 611		327.5 327 317 317 315 289.5 248.5	225
Q9b111 bombyx mori Q9b112 bombyx mori Q9b1369 calpodes et Q9vs97 drosophila Q9vv97 drosophila Q9vv87 mus musculu Q9qxz2 mus musculu	Q9BLL1 Q9BLL2 Q9BLS97 Q9VS97 Q9VV97 Q8VCS0 Q9QXZ2	11555555	194 208 195 186 190 530	32.0 31.8 31.4 31.4	336.3 36.5 329.5 329.5 329.5	17 18 19 20 21 21 23

ALIGNMENTS

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1 MLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHTAGS 60 :	Query Match 73.5%; Score 772; DB 6; Length 193; Best Local Similarity 73.7%; Pred. No. 1.1e-70; Matches 140; Conservative 21; Mismatches 27; Indels 2; Gaps	NCE 193 AA;	1 21 POTENTIAL.	EMBL; AJ409286; CAC84130.1; Signal.	EMBL; AJ131676; CAC19553.1;	Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.	"The peptidogifcan recognition protein is expressed in the lactating	Kappeler S.R., Farah Z., Puhan Z.;	SEQUENCE FROM N.A.	[2]	Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.	Recognition Protein.":	"Milk as a Source of Camel (Camelus dromedarius) Peptidoglycan	Kappeler S.R., Farah Z., Puhan Z.;	TISSUE-LACTATING MAMMARY GLAND:	SEQUENCE FROM N.A.	[1]	NCBI TRAXID=9838:			PGRP.	doglycar	20,	(TrEMBLrel. 16,	01-mar-2001 (TremBLrel. 16, Created)		O9GK12 PRELIMINARY: PRT: 193 AA.	ULT 1
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01-OCT-2000 (
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01-JUN-2002 (TrEMBLrel. 21, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
01-JUN-2002 (TrEMBLrel. 21, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Created)
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"Isolation, characterization, and antimicrobial properties of bovine oligosaccharide-binding protein: A microbicidal granule protein of eosinophils and neutrophils.";
J. Biol. Chem. 0:0-0(2002).
EMBL; AY083309; AAL87002.1; -
                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                               Peptidoglycan
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NCBI_TaxID=9913;
      NCBI_TaxID=10116;
                                                                                                                               Rattus norvegicus (Rat)
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(TremBLrel. 15, Last annotation)
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                                                                   Chordata;
Rodentia;
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Pred. No. 4.2e-65;
0; Mismatches 30;
                                                                   Craniata; Vertebrata; I
Sciurognathi; Muridae;
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SEQUENCE FROM N.A.

MEDLINE=21433985; PubMed=11461926;
Liu C., Xu Z., Gupta D., Dzlarski R.;
Liu C., Xu Z., Gupta D., Dzlarski R.;

"Peptidoglycan recognition proteins. a novel fam:
Innate immunity pattern recognition molecules.";

J. Biol. Chem. 276:34686-34694(2001).

EMBL; AY035376; AAK72484.1; -.
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF154114; AAF73252.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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STRAIN-SPRAGUE-DAWLEY; TISSUE-SPLEEN;
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                                                                                                                                                                                   TPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLYYEGRGWNFTGAHSGHLWNPMSIG 123
|| ||:|:|:|| ||:||:||:|| ||| ||:|::|
VSTDCQTVVRNIQSFHMDTRNFCDIGYHFLVGQDGGVYEGVGWHIQGSHT-YGFNDIALG 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWPHFK
                                               NWPHYR 189
                                                                                                                          ISFMGNYMDRVPTPQAIRAAQGILACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHLIQ 183
                                                                                                                                                                                                                                                                                  PLLLKEETCLDPQHPVMPRKVCPNIIKRSAWEARETHCPK-MNLPAKYVIIIHTAGTSCT 215
                                                                                                                                                                                                                                                                                                                PSLLRLGAAQETEDPA----CCSPIVPRNEWKALASECAQHLSLPLRYVVVSHTAGSSCN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIIQSWDHYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLIQNWPHYR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSIGITFMGDYSHRVPAKRALRAALNLLKCGVSEGFLRSNYEVKGHRDVQSTLSPGDQLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLFAWAPFPALLGLA-----DSCCF-VVPRSEWKALPSECSKGLKKPVRYVVISHTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124;
                                                                                         IAFIGYFVEKPPNAAALEAAQDLIQCAVVEGYLTPNYLLMGHSDVVNILSPGQALYNIIS
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340
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1 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 F
37611 MW;
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41.4%;
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                                                                                                                                                                                                                                                                                                                                                                                 43;
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Last annotation update)
rotein-I-alpha precursor
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                                                                                                                                                                                                                                                                                                                                                                              Score 441; DB 4;
Pred. No. 1.1e-36;
3; Mismatches 60
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8ADD5AA97B632076
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; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                 60;
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RESULT
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Bu Kambal, A., Edona S., Polland M., Venter J.C., Shu X., Smith H.O., Zheng L., J. (1900).
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9V4X2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wahrl J.F., Agbayani A., An H.-J., Andrews-Pfanakoch C., Baddwin D., Ballew R. Baser A. Bayerdala I. D., Andrews-Pfanakoch C., Baddwin D., Ballew R. Baser A. Bayerdala I. D., Andrews-Pfanakoch C., Baddwin D., Ballew R. Baser A. Bayerdala I. Ballew R. Baser A. Bayerdala I. Bayerdala II. Bayerdala I. Bayerdal
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000
01-MAY-2000
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                                                                            88
83
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IGYNFLIGGDGNVYEGRGWNVMGAHATN-WNSKSIGISFLGNYNTNTLTSAQITAAKGLL
                                                                       VGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNPMSIGISFMGNYMDRVPTPQAIRAAQGLL 147
                                                                                                                                                        IISKSEWGGRSATSKTSLANYLSYAVIHHTAGNYCSTKAACITQLQNIQAYHMDSLGWAD
                                                                                                                                                                                                  IVPRNEWKALASECAQHLSLPLRYVVVSHTAGSSCNTPASCQQQARNVQHYHMKTIGWCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P00806; 1LBA
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                                                                                                                                                                                                                                                                                                                            l Similarity
77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FBgn0043575; PGRP-SC2.
184 AA; 19829 MW;
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                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                              39.48;
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20,
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                              Score 414.5;
Pred. No. 2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0F99D04914B07238 CRC64;
                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 184;
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Smith H.O.,
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RESULT
Q9V3B7
ID 9V3B7
AC Q9
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Q96LB8
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Best Local
                                                                                                                                                                                                                                   Q9V3B7;
Q1-MAY-2000 (TrEMBLrel. 13, C
Q1-MAY-2000 (TrEMBLrel. 23, I
Q1-MAR-2002 (TrEMBLrel. 20, I
CG8577 protein and CG14746 pr
SC1B).
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HOMO Sapiens (Human),
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C., Xu Z., Gupta D., Dziarski R.;
"Peptidoglycan recognition proteins a novel family innate immunity pattern recognition molecules.";
J. Biol. Chem. 276:34686-34694(2001).
EMBL; AV035377; AAK72485.1;
InterPro; IPR002086; Aldehyde_dehydr.
                                                                                                                                                                                     PGRP-SC1A OR CG8577.3 OR CG14746.
Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
  STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                        Eukaryota;
Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 Q9V3B7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptidoglycan recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21433985; PubMed=11461926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 SDAVSRGQIVSGYILYGHRQVGSTECPGTNIWNEIRTWSNWKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IALGITFMGTFTGIPPNAAALEAAQDLIQCAMVKGYLTPNYLLVGHSDVARTLSPGQALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTCNISDECRLLVRDIQSFYIDRLKSCDIGYNFLVGQDGAIYEGVGWNVQGS-STPGYDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYVQPLLVKGENCLAPRQKTSLKKACPGVVPRSVWGARETHCPR-MTLPAKYGIIIHTAG
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                                                                                                                                             Neoptera;
                                                                                                                                                            Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                Drosophilidae;
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                                                                                                                                        Endopterygota;
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                                                                                                                                                                                                                                                           protein (Peptidoglycan-recognition protein-
                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                     erygota; Diptera;
Drosophila.
                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1488A166018A66AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                           Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                        Muscomorpha;
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Best Local S
Matches 79
Q95SQ9
Q95SQ9;
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"A family of peptidoglycan recognition proteins in the
Drosophila melanogaster.";
Proc. Natl. Acad. Sci. U.S.A. 97:13772-13777(2000).

EMBL; AE003836; AAF59052.1;
EMBL; AE003836; AAF59054.1;
EMBL; AF207542; AAG23736.1;
EMBL; AF207542; AAG23736.1;
FlyBase; FBgn0033327; PGRP-SCIb.
FlyBase; FBgn003376; PGRP-SCIa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                     143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDLINE=20558582; PubMed=11106397;
                                                                                                                                                          148
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                                                                                                                   NDAVNRGQLSSGYILYGHRQVSATECPGTHIWNEIRGWSHW
                                                                                                                                                                                                                                                                      VVSKAEWGGRGAKWTVGLGNYLSYAIIHHTAGSYCETRAQCNAVLQSVQNYHMDSLGWPD
                                                                                                                                                                                                                                                                                                        IVPRNEWKALASECAQHLSLPLRYVVVSHTAGSSCNTPASCQQQARNVQHYHMKTLGWCD
                                                                                                                                                                                                                       VGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNPMSIGISFMGNYMDRVPTPQAIRAAQGLL 147
                                                                                                                                                      ACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHLIQNWPHY
                                                                                                                                                                                           IGYNFLIGGDGNVYEGRGWNNMGAHAAE-WNPYSIGISFLGNYNWDTLEPNMISAAQQLL
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79; Conserv
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                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                20395 MW; F23F8D80A33541AC CRC64;
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                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                       Score 405.5;
Pred. No. 2.
                    PRT;
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                    185
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Q8WMF9;
01-MAR-2002
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01-DEC-2001
01-MAR-2002
GH07464p.
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NON_TER
                                                                                                                                                                                                                                                                     lactating mammary gland of camels.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ
EMBL; AJ310355; CAC83647.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0033327; PGRP-SClb. SEQUENCE 185 AA; 20336 MW; !
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Stapleton "
                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                                                Kappeler S.R.;
                                                                                                                                                                                                                                                                                                                                                                                     FISSUE-ADIPOSE TISSUE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptidoglycan
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                                                                                                                                                                                                                                                                                                                                    The peptidoglycan recognition protein, PGRP,
                    58 AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNPTGAHSGHLW 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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VVSKAEWGGRGAKWTVGLGNYLSYAIIHHTAGSYCETRAQCNAVLQSVQNYHMDSLGWPD 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGVAQGALRSNYVLXGHRDVQRTLSPGNQLYHLIQNWPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGYNFLIGEDGLYYEGRGWNFTGAHSGHLWNPMSIGISFMGNYMDRVPTPQAIRAAQGLL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDAVNRGQLSSGYILYGHRQVSATECPGTHIWNEIPGWSHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Pig).
                                                                                                                                                                                    86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 20, Creace, (TrEMBLrel. 20, Last sequence update) (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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86
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                                                                                                                                                                                  9517 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                               36.7%;
76.7%;
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                                                                                        Score 386; DB 6;
Pred. No. 7.8e-32;
1; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 403.5;
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Last annotation update
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                                                                                                                                                                                                                         PEPTIDOGLYCAN RECOGNITION
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                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                             databases
                                                                                          9
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Sus.
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ungall C.J.,
ng S., Wan K.,
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REPRESENTATION OF THE PROPERTY OF THE PROPERTY
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Q9VYX7
                                                                                                                                                                                                                                                                                                                                   RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Hallew R.M., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G.,
RA Hallew R.M., Basu A., Baxendale J., Bayraktarogiu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Balshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Chorry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Ling Y., Lin X.,
Lin X.,
RA Kimmel B.E., Ka
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01-MAY-2000
01-MAR-2002
                                                                                       STRAIN-DP CL CN BW;
MEDLINE-20558582; PubMed-11106397;
Merner T., Liu G., Kang D., Ekengren S.
"A family of peptidoglycan recognition
Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BERKELL:
MEDLINE-20196006; Pubmed-10731132;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila
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||:|:|||||||:||:||
61 NPLSLGISFMGNYMNRVPPARAIRAA
                                                               Natl.
                                                                                                                                                                                                                                                                                                                         287:2185-2195(2000).
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a; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; He
Neoptera; Endopterygota; Diptera;
¿Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TremBLrel. 13, Created)
(TremBLrel. 13, Last sequence update)
(TremBLrel. 20, Last annotation update)
tein (Peptidoglycan-recognition protein-SA)
                                                            Acad.
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                                                            U.S.A. 97:13772-13777(2000)
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a; Brachycera;
                                                                                                                         r H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insecta;
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RESULT
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Best Local S
Matches 76
                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                            Zhang W., Wan T., Cao X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF24518; AAF99599 1;
InterPro; IPR002086; Aldehyde_dehydr.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003486; AAF48056.1; --
EMBL; AF207541; AAG23735.1; --
EMBL; AF207540; AAG23734.1; --
EMBL; AF075293; AAL68160.1; --
EMBL; AF075293; AAL68160.1; --
ELYBase; FBg00030310; PGRP-SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Cr
01-MAR-2001 (TrEMBLrel. 16, La:
01-JUN-2001 (TrEMBLrel. 17, La:
Hypothetical 40.0 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
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Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Change M., Chavez C., Dorsett V., Dresnet D., Farfan D., Frise George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park
                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 368 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9нD75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9HD75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 QNWPHYRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134
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                                                    105
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                                GWNFTGAHSGHLWNPMSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKG
                                                                                              MTLPAKYGIIIHTAGRTCNISDECRLLVRDIQSFYIDRLKSCDIGYNFLVGQDGAIYEGV
                                                                                                                            LSLPLRYVVVSHTAGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIAFIGNEVDKLPSDAALQAAKDLLACGVQQGELSEDYALIAGSQVISTQSPGLTLYNEI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAWALPSILRIGAAQETEDPACCSPIVPRNEWKALASECAQHISLPLRYVVVSHTAGSSC
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                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
STPGYDDIALGITFMGTFTGIPPNAAALEAAQDLIQCAMVKGYLTPNYLLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Primates;
                                                                                                                                                                                                                                                                                          40020 MW;
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                                                                                                                                                                                                                    35.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16, Created)16, Last sequence up17, Last annotation
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Pred. No. 1.2e
34; Mismatches
                                                                                                                                                                                      Score 371.5; DB 4
Pred. No. 1.5e-29;
3; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                          1E74970732A5DAFD CRC64;
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No. 1
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Yu C., Lewis S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata; Euteleostomi;
i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5;
1.2e-30;
76;
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01-MAR-2002 (TrEMBLrel. 20,

01-MAR-2002 (TrEMBLrel. 20,

01-MAR-2002 (TrEMBLrel. 20,

Peptidoglycan recognition p.

Bombyx mori (Silk moth).
                                                                                                                                                                                                                                                                  01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                              SEQUENCE FROM N.A.

PubMed-11872802;

Choe K.-M., Werner T., Stoven S., Hultmark D., Anderson K.V.

"Requirement for a Peptidoglycan Recognition Protein (PGRP)

Activation and Antibacterial Immune Responses in Drosophila.

Science 296:359-362(2002).

SCHERCE 500 AA; 54094 MW; A0459DE723A8C720 CRC64;
                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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Kim S.H., Lee H.S., Kim J.W., Lee Y.S., Ryu K.S., Jun Y.

Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases

EMBL; AF441723; AAL32058.1; -

SEQUENCE 195 AA; 21478 MW; 17F85F01B1DA035E CRC64;
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Bombycoidea; Bombycidae; Bombyx.
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LPINRVVISHTAAEGCESREVCSARVNVVQSFHMDSWGWDHIGYNFLVGGDGRVYEGRGW
            LPLRYVVVSHTAGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGW
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Pred. No. 1.5e
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Pred. No. 1
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ota; Diptera; Brachycera;
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Q96N74;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ31320 fis, clone LIVER1000542, moderately s.
Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDITINE-21433985; PubMed-11461926;
Liu C., Xu Z., Gupta D., Dziarski R.;

"Peptidoglycan recognition proteins: a novel fam.
innate immunity pattern recognition molecules.";
J. Biol. Chem. 276:34666-34694(2001).
                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                      musculus TAGL-alpha mRNA.
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Mammalia; Eutheria;
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Metazoa; Primates; (
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Search completed: November 12, 2002, 02:26:31 Job time: 146 secs
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                                                                                                                                                                                                                                                                                                                                                              Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
*NEDO human CDNA sequencing project.";
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK055882; BAB71034.1; -
SEQUENCE 634 AA; 67970 MW; 93E2032F3CE38E70 CRC64;
                                                                      379 CPAIHPRCRWGAAPYRGRPKLLQLPLGFLYVHHTYVPAPPCTDFTRCAANMRSMQRYHQD 438
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2002 Compugen Ltd
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
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    AAY00771
AAB254022
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AAB256964
AAY96964
AAY99400
AAB66149
AAW23722
AAY00770
AAW23723
AAY64935
                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (without alignments)
177.978 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    908470
Human tag7 clone p
Human PRO1269 prot
Htag7 protein enco
Chondrosarcoma pep
Human PRO1269 (UNQ
Protein of the inv
Bovine granulocyte
Mouse tag7 clone p
Murine granulocyte
Human 5' EST relat
                                                                                                                                                                                                                                   Description
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#7909	591	22	53	12.1	127.5	01
enc	ABB42485	22	53	•	127.5	-
Human taq7 clone p	AAY00774	20	26	•	138	w
Drosophila melanog	ABB61601	22	505	•	147.5	١٠
Human Zgpal domain	AAE00694	22	132	•	177.5	
n peptid	AAY72663	22	174	•	193	_
o.	ABG27581	22	363	18.7	196.5	•
C glutamicum prote	AAG92931	22	683	•	202	~
	ABB60590	22	280	•	229.5	٦.
Drosophila melanog	ABB60610	22	611	•	248.5	٠,
Drosophila melanog	ABB64595	22	182	٠	289.5	٠.
ρr D'	AAY76124	21	244	•	316.5	_
Keratinocyte pepti	AAY96962	21	243	٠	316.5	_
	ABB69711	22	215	•	317	
	ABB60644	22	337	•	327	•
Amino acid sequenc	AAW37836	19	173	٠	328.5	_
Recombinant peptid	AAW37834	19	173	•	328.5	_
Drosophila melano	ABB64581	22	190	٠	329.5	_
ĭ	ABB61200	22	186	31.4	330	-
Murine peptidoglyc	AAY72664	22	530	•	332.5	٠.
hila	ABB64149	22	345	٠	347	٠.
acid	AAW37835	19	196	٠	347.5	
Amino acid sequenc	AAW37837	19	196	•	347.5	_
acid	AAG65915	22	634	•	348.5	
acid sec	AAG65916	22	576	•	348.5	•
protein clo	AAY94863	21	363	٠	348.5	_
ling tis	AAY96963	21	368	•	371.5	_
melano	ABB70267	22	203	٠	379	~
נם	ABB69758	22	185	•	405.5	_
phila melan	ABB59234	22	185	٠	405.5	Ψ,
ful	AAE00692	22	375	٠	413	Ψ.
_	ABB53272	23	369	•	413	-
ful.	AAE00693	22	369	39.3	413	w
Human polypeptide	ABB53271	23	241	•	413	
Drosophila melanog	97	22	184		414.5	

ALIGNMENTS

RESULT 1 AAY00771

AAY00771 standard; Protein; 191 AA

18-MAY-1999 AAY00771;

(first entry)

New nucleic acid encoding tag7 - used to inhibit tumour growth and induce apoptosis, for treatment of carcinoma, sarcoma, melanoma and leukaemia WPI; 1999-120887/10. N-PSDB; AAX21820. Georgiev G, 11-JUL-1997; Tag7; tumour growth inhibitor; mammalian tumour; carcinoma; sarcoma; melanoma; leukaemia; apoptosis inducer; human. Human tag7 clone protein sequence 10-JUL-1998; 21-JAN-1999. WO9902686-A1 Homo sapiens (BOEH) BOEHRINGER INGELHEIM INT GMBH. Kiselev 97US-0893764. 98WO-EP04287. Ś Ostermann E, Prokhorchouk E;

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RESULT 2
AAB24022
ID AAB2
XX AAB2
XX AAB2
XX AAB2
XX Huma
XX Huma
XX Iden
XX I
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Best Local
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                                                                                                                                                                            08-MAR-1999;
01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is the human tag7 of the invention. Cells containing the tag7 DNA sequence are used to express recombinant tag7. Tag7 is used to produce and purify antibodies; to inhibit growth of mammalian tumours, especially for treating carcinoma (of liver, ovary, breast, cervix, lung, prostate, colon/rectum, bladder, testis, stomach, pancreas, mouth, head and neck, squamous cell carcinoma or teratocarcinoma), sarcoma (Kaposi's, osteo- or fibro-sarcomas), melanoma or leukaemia; and as a molecular redight marker. The tag7 polypeptide inhibits tumour growth and induces appotosis. The tag7 coding sequences are also useful as probes for gene mapping and detection of tag7 gene expression, and as primers. Antibodies against tag7 are used as reagents for detecting tag7; as an antagonist of tag7; for isolating tag7 and therapeutically to inhibit or delay tumour
                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PRO1269 protein sequence SEQ ID NO:7.
     N-PSDB;
                                                                        Botstein D,
                                                                                                                                                                                                                                                                                                                                      02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                          14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200053750-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2001
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                           2000-594320/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour;
  AAC58104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 AA;
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ilarity 100.0%;
Conservative (
                                                                        Goddard
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99US-0162506.
99WO-US28313.
99WO-US28634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis; neoplastic disease; proliferation;
; tumourigenesis; anticancer; detection.
                                                                                                                                                                                                                                                                                   99WO-US05028
                                                                                                                                                                                                                                                                                                                                      99WO-US28551
                                                                                                                            INC.
                                                                        P
                                                                        Gurney
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Pred. No. 2.6
0; Mismatches
                                                                        ΑĿ,
                                                                        Roy
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                                                                        Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                        Ç
                                                                        Wood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells. Increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), especially the antibodies, or an antisense oligonucleotide which hybridises to genes encoding (I), can be used to inhibit tumour growth, preferably by inducing cell death. Methods from the present invention can be used to identify compounds which inhibit the biological activity of (I). AAC58103 to AAC58103 represent PCR primers and hybridisation probes used in examples from the present invention for human PRO sequences. AAC58103 to AAC5812 and AAB24021 to AAB24040 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                              multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an antibody that binds to a human protein (I) selected from: PRO315; PRO1269; PRO1410; PRO3155; PRO197; PRO3567; PRO1925; PRO1927; PRO3567; PRO1925; PRO1927; PRO3567; PRO1926; PRO2038; and PRO2262. (I) has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibodies specific for PRO polypeptides, used to diagnose and the growth of tumors in mammals, and to identify inhibitors of polypeptide activity or expression - {\sf polypeptide}
                                                                                                                  melanoma; lymphoma;
                                                                                                                            Crohn's disease; nephritis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myoc
                                                                                                                                                                                                antirheumatic, dermatological; antiproliferative; antiarteriosclerotic;
anticancer; vulnerary; antiviral; antibacterial; antifungal;
                                                                                                                                                                                                                                                                  Htag7 protein encoded by human secreted protein gene #8
                                                                                                                                                                                                                                    Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
                                                                                                                                                                                                                                                                                                         21-NOV-2000
                                                                                                                                                                                                                                                                                                                                             AAB25583;
                                                                                                                                                                                                                                                                                                                                                                           AAB25583 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                  immune disorder; Addison's disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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A
                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                  wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1051; DB 21; 100.0%; Pred. No. 2.7e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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WO200029435-A1 Homo sapiens

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Chondrosarcoma peptidoglycan recognition protein-like protein.
                                    31-OCT-2000
                                                                   AAY96964;
                                                                                                 AAY96964 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-inflammatory; antiarthritic; antirheumatic, dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dependent on the tissues in which they are expressed. Examples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotide sequences encoding them. The polynucleotide sequences given in AAA80606-A80623 encode the 12 secreted protein sequences given in AAB25576-B25593. The human secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the
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                                                                                                                                                                                  LIQNWPHYRSP 196
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Peptidoglycan recognition protein-like protein; PGRP; PGRP-C; regulator; chondrosarcoma; immunosuppressive; antibacterial; anti-apoptotic; tumour necrosis factor; TNF; anti-infectious; mononuclear phagocyte; inhibitor; protein co-ordinate data.
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22-DEC-1999; 99WO-US30736

23-DEC-1998; 98US-0113809

(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Ruben SM, Young PE, Olsen SH

2000-452414/39. DB; AAA51719.

Polynucleotide encoding peptidoglycan recognition protein-like protein, antibodies specific to it useful for preventing, treating conditions e.g. endotoxic shock and auto-immune disorders and infections in mammal

Claim 11; Fig 3; 191pp; English

Novel human peptidoglycan recognition protein-like proteins (PGRP) expressed by keratinocytes (PGRP-K), wound healing tissues (PGRP-W) or chondrosarcoma tissue (PGRP-C) are disclosed. The PGRP DNA and proteins are useful for preventing, treating or ameliorating a medical condition in a mammal (claimed). PGRP is useful in augmenting the immune immune system activation. Antibodies or antagonists directed against these proteins may be useful in reducing or eliminating disorders associated with tumour necrosis factor (PWF) and TMF-like cytokines, such as endotoxic shock and autoimmune disorders and for treating condition in a mammal (claimed). PGRP is useful in augmenting the imsystem in such areas as immune recognition, antigen presentation and Novel human peptidoglycan recognition fibrosis including silicosis, sarcoidosis and idiopathic

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Query Match Best Local S Matches 191 itch 100.0%; sal Similarity 100.0%; 191; Conservative (Score 1051; DB 21; Pred. No. 2.7e-104; ; Mismatches 0; Indels Length 196; 0 Gaps

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                                                                                                                                                                                                                                                                                                   AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
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17-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                           New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
                  Protein of the invention #61.
                                  02-APR-2001
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DB; AAA37082.
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transmembrane; gene therapy.
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Gao W,
Pan J,
AAW23722;
                          AAW23722 standard;
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                                                                                                      LIQNWPHYRSP
                                                                                                                                                               SIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYH
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Goddard A,
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e CK, Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 122;
                                                                                                                                                                                                                                                                                                                                                                                                          196
                                                                                                                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                    animals or knockout animals which are in turn useful for and screening of therapeutically useful reagents. acids may also be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US28551.
99WO-US30095.
2000WO-US00219.
2000WO-US00376.
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99WO-US28313
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99WO-US20111
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Godowski PJ,
Roy MA, Smith
                          Protein; 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ssnoyers L, Eaton DL, Fi
ki PJ, Grimaldi CJ, Gui
Smith V, Stewart TA,
Wood WI;
                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                            Score 1051; DB 22;
Pred. No. 2.7e-104;
; Mismatches 0;
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Gurney AL,
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                                                                                                                                                                                                                              Escherichia coli, Candida albicans, Salmonella typhimurium and C. neoformans (claimed). They can be used in human or veterinary medicine (particularly to treat disorders associated with lipopolysaccharides, e.g. sepsis and endotoxaemia) or as preservatives in food products or in water supplies (claimed). They can also be applied to crops to reduce post-harvest spoilage or expressed in transgenic plants to increase their disease resistance. They have low immunogenicity. Carboxamidated analogues of BGP-A and MGP-A may also be used.
                                                                                                                                                                                                                                                                                                                                                     This protein comprises the precursor (see AAW23722) of a novel, claimed antimicrobial peptide from bovine neutrophils, designated bovine granulocyte peptide A or BGP-A (see AAW23724). Its amino aci sequence was deduced from a cDNA clone (see AAT9509) obtained from bovine bone marrow. BGP-A and the murine homologue, MGP-A (see AAW23725), exhibit activity against Gram-positive and Gram-negative bacteria, fungi and viruses, specifically Staphylococcus aureus,
                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial (poly)peptide(s) from bovine and murine granulocytes useful therapeutically, as preservatives for food, in water treatment and in agriculture
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Fig 4; 56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fungicide; antiprotozoa;
                 123
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                                                                                                                                                                Local Similarity
GISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHLI
                               LAWALPSILRIGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHTAGSSC
                                                       NTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNPMSI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        granulocyte peptide A; BGP-A.
                                                                                                                                                                                                        190 AA;
                                                                                                                                                     Conservative
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                                                                                                                                                                68.2%;
70.1%;
                                                                                             -CGSIVSRGKWGALASKCSQRLRQPVRYVVVSHTAGSVC
                                                                                                                                                 20;
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Pred.
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                                                                                                                                                  Mismatches
                                                                                                                                                 e 717; DB 18;
. No. 1.5e-68;
ismatches 30;
                                                                                                                                                                            Length 190;
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                                                                                                                                                                 Matches
                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                             This sequence is the murine tag7 of the invention. Cells containing the tag7 DNA sequence are used to express recombinant tag7. Tag7 is used to produce and purify antibodies; to inhibit growth of mammalian tumours, especially for treating carcinoma (of liver, ovary, breast, cervix, lung, prostate, colon/rectum, bladder, testis, stomach, pancreas, mouth, head and neck, squamous cell carcinoma or terratocarcinoma), sarcoma (Kaposi's, osteo- or fibro-sarcomas), melanoma or leukaemia, and as a molecular weight marker. The tag7 polypeptide inhibits tumour growth and induces apoptosis. The tag7 polypeptide inhibits tumour growth are serviced mapping and detection of tag7 gene expression, and as primers. Antibodies against tag7 are used as resgents for detecting tag7; as an antagonist of tag7; for isolating tag7 and therapeutically to inhibit or delay tumour metagraters.
                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 19; Fig 1; 138pp; English.
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N-PSDB; AAX21819.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tag7; tumour growth inhibitor;
melanoma; leukaemia; apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse tag7 clone protein sequence
                                                                                                                                                                                                                                                       metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          induce apoptosis,
leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding tag7 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BOEH ) BOEHRINGER INGELHEIM INT GMBH
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                  121
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                                                                                                                      1 MLLAWALPSLLRIGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHTAGS
SIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYH
                                                          SCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNPM 120
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                                            FCNSPDSCEQQARNVQHYHKNELGWCDVAYNFLIGEDGHVYEGRGWNIKGDHTGPIWNPM
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                                                                                                                                                                 al Similarity
127; Conserv
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                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding tag7 - used to inhibit tumour growth and for treatment of carcinoma, sarcoma, melanoma and
                                                                                                                                                                            65.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ostermann
                                                                                                                                                               21;
                                                                                                                                                            Score 692; DB 20;
Pred. No. 6.9e-66;
(1; Mismatches 33;
                                                                                                     -CSFIVPRSEWRALPSECSSRLGHPVRYVVISHTAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mammalian tumour; carcinoma; sarcoma;
inducer; mouse.
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Matches 125
                                                                                   Escherichia coli, Candida albicans, Salmonella typhimurium and C. neoformans (claimed). They can be used in human or veterinary medicine (particularly to treat disorders associated with lipopolysaccharides, e.g. sepsis and endotoxaemia) or as preservatives in food products or in water supplies (claimed). They can also be applied to crops to reduce post harvest spoilage or expressed in transgenic plants to increase their disease resistance. They have low immunogenicity. Carboxamidated analogues of MGP-A and BGP-A may also be used.
                                                                                                                                                                                                                   This protein comprises the precursor of a novel, claimed antimicrobial peptide from murine neutrophils, designated murine granulocyte peptide A or MGP-A (see AAM23725). Its amino acid sequence was deduced from a cDNA clone (see AAT9510) obtained from murine bone marrow. MGP-A and the bovine homologue, BGP-A (see AAW23724), exhibit activity against Gram-positive and Gram-negative bacteria, fungi and viruses, specifically Staphylococcus aureus,
                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial (poly)peptide(s) from bovine and murine granulocytes useful therapeutically, as preservatives for food, in water treatment and in agriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial peptide; antibiotic; antibacterial; antifungal; fungicide; antiprotozoa; protozoacide; antiviral; virucide; murine granulocyte peptide A; MGP-A; preservative; sepsis;
                                                                                                                                                                                                                                                                                                                                             Claim
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N-PSDB; AAT78510.
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Local Similarity
wes 125; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIQSWEHYR 181
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                                                                                                                                                                                                                                                                                                                                        9; Fig 5; 56pp; English
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                                                            181
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/note- "MGP-A antimicrobial peptide
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             62.9%;
            Score 661.5; DB 1
Pred. No. 1.3e-62;
                           DB 18;
 Indels
                          Length 181;
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Sequences, corresponding to human secreted proteins. AAY64651 to CAX65438 represent the EST-related proteins corresponding to AAZ42265 to AAZ43052. The 5' ESTs can be used for producing secreted human gene C products. They can be used to identify and isolate 5' untranslated c regions (UTRs) and upstream regulatory regions which control the C location, development stage, rate, and quantity of protein synthesis, as c well as stability of mRNA. The ESTs are also useful as probes for C chromosome mapping, and to obtain full length cDNA clones. The ESTs can CC diagnostic procedures to identify individuals, or in CC diagnostic procedures to identify individuals having genetic diseases C resulting from abnormal gene expression. The products may also be used in CC gene therapy protocols. The nucleic acids encoding signal peptides can be CC used for directing extracellular secretion of a polypeptide or the CC into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have
                                                                                                                                                                                                                                                                                                                                                   Novel secreted protein 5' expressed diagnostic, forensic, gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
gene therapy; chromosome mapping; upstream regulatory sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY64935;
                                                                                                                                                                                                                                                                                    AAZ42265 to AAZ43075 represent novel 5' expressed sequence
                                                                                                                                                                                                                                                                                                                    Claim 3; Page 685; 837pp; English.
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28-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGITFMGNFMDRV-RKAALRAALNLLESGVSRGFLRSNYEVKGHRDVQSTLSPGDQLYQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MILAWALPSILRIGAAQETEDPACCSPIVPRNEWKALASECAQHISLPLRYVVVSHTAGS
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98US-0069047
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                                                                                                                                                                                                                                                                                                                                               sequence tag sequences used and chromosome mapping proce
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                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventuaseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                            Sequence
                                                                             specification,
                                                                                                                                                                                           Disclosure; SEQ ID NO 36063; 21pp + Sequence Listing;
                                                                                                                                                                                                                            New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                       23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             valuable.
sequences
                                                                                   (ABB57737-ABB72072).
The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                 (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical.
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                                                               ftp.wipo.int/pub/published_pct_sequences.
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DB; ABL13860.
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   77; Conser
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2000US-0614150
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           39.4%;
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                                                                                                                                                                                                                                                                                            PWD,
                                                                                                                                                                                                                         detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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           Score 414.5;
Pred. No. 3.8
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Pred. No. 6.1e-45;
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      The invention relates to an isolated polypeptide comprising a 277, 480 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026, 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255, 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as given in the specification. The polypeptides, modulators of the polypeptides and antibodies against the polypeptides are useful for treating diseases such as neurological and psychiatric diseases. Including Alzheimer's, parasupranuclear palsy, Huntington's disease, myotonic dystrophy, anorexia and depression; cardiovascular diseases including congestive heart failure, Hodykin's disease and myocardial pulmonary disease, cystic fibrosis and adult respiratory distress enhancements of the service constructive surfarements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-APR-2000; 2
11-MAY-2000; 2
25-MAY-2000; 2
26-MAY-2000; 2
                                                                                                                                                                                                                     Claim 1; Page 79;
                                                                                                                                                                                                                                                           Novel polypeptides and polynucleotides useful as a vaccine for preventing and treating diseases associated the polypeptide, e.g. Alzheimer's disease, dyslipidemia, obesity, diabetes, infertility,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory; antilipaemic; hepatotropic; virucide; antidiabetic; nephrotropic; anorectic; cytostatic; vaccine; neurological disease; cardiovascular disease; respiratory disease; liver disease; renal disease; skeletal muscle disease; gastrointestinal disease; placental disease; testicular cancer; male fertility; pancreatic disease;
                                                                                                                                                                                                                                                     asthma, amnesias
                                                                                                                                                                                                                                                                                                                                                                                                                           (SMIK )
                                                                                                                                                                                                                                                                                                                                                                                           Agarwal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; nootropic; neuroprotective; anticonvulsant; antidepressant; neuroleptic; tranquiliser; antiarrhythmic; cardiant; antiasthmatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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DB; ABA90336.
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2000US-203336P.
2000US-207087P.
2000US-207546P.
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hypercholesterolaemia,
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Matches 76
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                                                                                                                                                                                                                                                                                                               Human; granulocyte peptide A; GP-A; Zgpal; cytostatic; antiinflammatory; vulnerary; dermatological; anti-microbial; gastrointestinal disease; pulmonary; dental carries; periodontal disease; gene therapy; AIDS; Acquired Immune Deficiency Syndrome; epithelial wound; cystic fibrosis; infection; urinary tract; respiratory; vaginal; lung; skin; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                Human full length granulocyte peptide homolog Zgpal protein #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                     Domain
                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                          Region
                                                                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                                     rectal;
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                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the invention.
            /label=
117..122
                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                      /label
                                                                                                                                                 /label
                                                                                                                                                                            /label= Mature_full_length_Zgpal_protein_#2
/note= "This region functions as an immunog
                                                                                                                                                                                                                                                                                                     chromosome
                                                                               /label= Immunogenic_epitope
/note= "This region is specifically claimed in
                                                                                                                                                                                                                    /label=
                                                    label-
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                                                                                                                                                 Immunogenic_epitope
                                                                                                                                                                                                                    Signal_peptide
Hydrophilic_region
                                                    Hydrophilic_region
                                                                                                                       Domain_1
                         Immunogenic_epitope
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Pred. No. 7.9e
$2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23;
1.9e-36;
nes 66;
                                                                                                                                                                            as an immunogenic
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                                                                                                                                                                            epitope'
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The present sequence is human full length granulocyte peptide (GP-A) CC homolog, Zgpal protein. Zgpal gene is located on human chromosome 1. CC zgpal polypeptides are useful for producing antibodies which are useful CC for detecting cancer. Zgpal polypeptides having anti-microbial activity are useful for treating dental carries, periodontal disease, thrush, CC detecting cancer. Zgpal polypeptides having anti-microbial activity are useful for treating dental carries, periodontal disease, thrush, CC questrointestinal disease, urinary tract infections, vaginal infections, caquired immune deficiency syndrome (AIDS) and CC useful for treating dental threat in the fusion CC proteins associated with cystic fibrosis and prevention of CC infection in skin and other epithelial wounds. Zgpal-cytokine fusion CC proteins are useful for enhancing in vivo killing of target tissues (epithelial cancers, and more specifically lung, ovarian and rectal CC cancers). Zgpal polypeptides, fragments, fusion proteins or agonists are useful in in vitro studies of exogenous microorganism infections such as bacterial, viral or fungal infection and also to study epithelial cell cell cells of cancers. Zgpal sequences are useful so diagnostics in RNA or CC ansers. Zgpal sequences are useful as diagnostics in necl cancers. Zgpal sequences are useful as diagnostics in neclic manual cancers are useful as diagnostics in cells. Squal antibodies are useful as diagnostics in neclic and as probes or primers to clone 5 non-coding cells regions of a zgpal gene. Zgpal antibodies are useful for tagging cells
                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Page 109-110; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  New granulocyte peptide homolog, zgpal polypeptide, for research applications, diagnosis and treatment of cancer, periodontal, gastrointestinal disease, urinary tract, skin and lung infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conklin
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12-JUL-2000;
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2000US-0218070.
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This region is specifically claimed
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RESULT 1
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Best Local
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   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       that express neutralizing in vitro and
                                Novel polypeptides and polynucleotides useful as a vaccine for preventing and treating diseases associated the polypeptide, e Alzhelmer's disease, dyslipidemia, obesity, diabetes, infertil
                                                                                                                                                      (SMIK )
                                                                                                                                                                                                                                                                                                                                          Human; nootropic; neuroprotective; anticonvulsant; antidepressant; neuroleptic; tranquiliser; antiarrhythmic; cardiant; antiasthmatic; antiinflammatory; antilipaemic; hepatotropic; virucide; antidiabetic; nephrotropic; anorectic; cytostatic; vaccine; neurological disease; cardiovascular disease; respiratory disease; liver disease; renal disease; skeletal muscle disease; gastrointestinal disease; placental disease; testicular cancer; male fertility; pancreatic disease.
                                                                                                                                                                                         27-APR-2000; 2000US-199963P.
11-MAY-2000; 2000US-203336P.
25-MAY-2000; 2000US-207087P.
26-MAY-2000; 2000US-207546P.
                                                                                                                                                                                                                                                                            01-NOV-2001
                                                                                                                                                                                                                                                                                                   W0200181363-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB53272 standard; Protein;
                                                                                                                                 Agarwal
                                                                                                                                                                                                                                                    26-APR-2001; 2001WO-US13360
                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
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                                                                                 2002-041392/05.
DB; ABA90337.
                                                                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIISTWPHFK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSIGISEMGNYMDRVPTPQAIRAAQGLLACGYAQGALRSNYVLKGHRDVQRTLSPGNQLY 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RTCNISDECRLLVRDIQSFYIDRLKSCDIGYNFLVGQDGAIYEGVGWNVQGS-STPGYDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLIQNWPHYR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYYEGRGWNFTGAHSGHLWNP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide #12
                                                                                                                    Xie
                         amnesias
                                                                                                                                                      SMITHKLINE BEECHAM
SMITHKLINE BEECHAM
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  Page 79-80;
                                                                                                                   Murdock
Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  zgpal, for screening expression libraries and as antibodies or as antagonists to block zgpal activity in vivo. Zgpal gene is also useful in gene therapy.
                                                                                                                                PR,
116pp;
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                                                                                                                               Rizvi SK,
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English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 413; DB 22;
Pred. No. 1.4e-35;
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                                                                                                                              2,
                                ptide, e.g.
infertility,
                                                                                                                              Kabnick KS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                Human; granulocyte peptide A; GP-A; Zgpal; cytostatic; antiinflammatory; vulnerary; dermatological; anti-microbial; gastrointestinal disease; pulmonary; dental carries; periodontal disease; gene therapy; AIDS; Acquired Immune Deficiency Syndrome; epithelial wound; cystic fibrosis; infection; urinary tract; respiratory; vaginal; lung; skin; cancer; ovarian; rectal; chromosome 1.
                                                                                                                                                                                                                                                                                                                                                                        Human full length granulocyte peptide homolog Zgpal protein #1.
                                    Protein
                                                                                                         Key
                                                                               Peptide
                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE00692 standard; Protein; 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    male reproductive diseases including low testosterone and male infertility; and disease of pancreas including diabetic ketoacidosis. Type 1 and 2 diabetes and obesity. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loca L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYVOPLLVKGENCLAPROKTSLKKACPGVVPRSVWGARETHCPR-MTLPAKYGIIHTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIISTWPHFK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLIQNWPHYR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IALGITFMGTFTGIPPNAAALEAAQDLIQCAMVKGYLTPNYLLVGHSDVARTLSPGQALY 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLY 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP 119
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76; Conserv
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                              /label=
18..375
                                                                             Location/Qualifiers
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Mature_full_length_Zgpal_protein_#1
                                                   Signal_peptide
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Pred. No. 1.4e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 369;
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The present sequence is human full length granulocyte peptide (GP-A) homolog, Zgpal protein. Zgpal gene is located on human chromosome 1. Zgpal polypeptides are useful for producing antibodies which are useful for detecting cancer. Zgpal polypeptides having anti-microbial activity are useful for treating dental carries, periodontal disease, thrush, detecting cancer. Zgpal polypeptides having anti-microbial activity are useful for treating dental carries, periodontal disease, thrush, detecting cancer. Zgpal polypeptides having anti-microbial activity are useful for treating dental carries, periodontal disease, thrush, gastrointestinal disease, uninary tract infections, vaginal infections,
polypeptides are useful for detection of zgpal polypeptide, mRNA or anti-zgpal antibodies, thus serving as markers for detecting genetic diseases or cancers. Zgpal sequences are useful as diagnostics in forensic DNA profiling and as probes or primers to clone 5 non-coding regions of a zgpal gene. Zgpal antibodies are useful for tagging cells that express zgpal, for screening expression libraries and as neutralizing antibodies or as antagonists to block zgpal activity in vitro and in vivo. Zgpal gene is also useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                            proteins are useful for enhancing in vivo killing of target tissues (epithelial cancers, and more specifically lung, ovarian and rectal cancers). Zgpal polypeptides, fragments, fusion proteins or agonists are useful in in vitro studies of exogenous microorganism infections such as bacterial, viral or fungal infection and also to study epithelial cell defensing induction in cell culture. Zgpal antibodies, polynuclectides and content of the content of the culture of the content of the culture of the content of the culture of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New granulocyte peptide homolog, zgpal polypeptide, for research applications, diagnosis and treatment of cancer, periodontal, gastrointestinal disease, urinary tract, skin and lung infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-OCT-1999; 99US-0160712.
12-JUL-2000; 2000US-0218070.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              respiratory infections, acquired immune deficiency syndrome (AIDS) and lung infections associated with cystic fibrosis and prevention of infection in skin and other epithelial wounds. Zgpal-cytokine fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14; Page 105-106; 114pp; English.
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/note= "This region is specifically claimed in claim 18"
58..189
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47..52
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L57..162
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365
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                                                                                            246 RTCNISDECRLLVRDIQSFYIDRLKSCDIGYNFLVGQDGAIYEGVGWNVQGS-STPGYDD 304
                                                                                                                                              187
                      180 HLIQNWPHYR 189
                                                                                                          4 AWALPSILR----LGAAQETEDPACCSPIVPRNEWKALASECAQHISLPLRYVVVSHTAG
                                                           MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLY 179
                                                                                                                                           SYVQPLLVKGENCLAPRQXTSLKKACPGVVPRSVWGARETHCPR-MTLPAKYGIIIHTAG 245
NIISTWPHFK
                                             TALGITEMGTETGIPPNAAALEAAQDLIQCAMVKGYLTPNYLLVGHSDVARTLSPGQALY
                                                                                                                                                                                              76;
                                                                                                                                                                                              Conservative
374
                                                                                                                                                                                                       39.3%;
                                                                                                                                                                                             42;
                                                                                                                                                                                                       Score 413; DB 22;
Pred. No. 1.4e-35;
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                    Length
                                                                                                                                                                                              Indels
                                                                                                                                                                                                                      375;
                                                                                                                                                                                             6,
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Search completed: November 12, 2002, 02:22:14
Job time: 144 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
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1051
1 MLLAWALPSILRLGAAQETE......ISPGNQLYHLIQNWPHYRSP 191
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Gapop 10.0 , Gapext 0.5
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pir3:*
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T35329
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45	44	43	42	41	40	39	38	37	36	35	34	ω	32	31	30
_. 72	72.5	72.5	72.5	73	73	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	74
6.9	6.9	6.9	6.9	6.9	6.9	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0
566	628	532	378	533	393	1733	1159	717	717	641	439	439	420	244	1477
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н83037	AG1469	A72694	B55580	D75220	JE0180	B45344	T02866	S31034	S31035	G85043	T43585	A55520	H75395	AC3533	T18534
ureasė alpha subun	transporter homolo	hypothetical prote	carbamoyl-phosphat	hypothetical prote	phosphopentomutase	probable nuclear a	hypothetical prote	retrovirus-related	retrovirus-related	hypothetical prote	yops secretion pro	yscN protein - Yer	ABC transporter, p	l-fuculose phospha	protein-tyrosine k

ALIGNMENTS

		·			
RESULT 2 135303 hypothetical protein SC5F7.14c - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999 C;Accession: T35303 R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999 A;Reference number: Z21574	Qy 118 MPMS1GISEMGNYMDRYPTPQAIRAGGUAG		Query Match 21.3%; Score 224; DB 2; Length 539; Best Local Similarity 29.0%; Pred. No. 1.3e-13; Batches 64; Conservative 31; Mismatches 82; Indels 44; Ga	A;Accession: G/0520 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-539 <col/> A;Cross-references: GB:Z97188; GB:AL123456; NID:g3261805; PIDN:CAB10019.1; PID:e13000 A;Experimental source: strain H37Rv C;Genetics: A;Gene: csp	G70520 probable csp protein - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Decies: Mycobacterium tuberculosis C;Caccession: G70520 C;Accession: G70520 C;Cccession: G70520 C;Cccnor, R; Davies, R; Devili, K; Fellwell, T; Gentles, S; Hanris, N; Holroyd, Connor, R; Davies, R; Devili, K; Fellwell, T; Gentles, S; Hamlin, N; Holroyd, Rajandream, M.A; Rogers, J; Rutter, S; Seeger, K; Skelton, S; Squares, S. Raindream, M.A; Rogers, J; Rutter, S; Seeger, K; Skelton, S; Squares, S. A;Authors: Sqares, R; Sulston, J.E.; Taylor, K; Whitehead, S; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete gence A;Reference number: A70500; MUID:98295987; PMID:9634230

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A; Accession: T35303
A; Status: preliminary; translated fro
A; Molecule type: DNA
A; Residues: 1-308 <SEE>
A; Cross references: EMBL: AL096872; PI
A; Experimental source: strain A3(2)
C; Genetics:
A; Gene: SCOEDB: SC5F7.14c
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: 3.
C;Superfam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: gene 3.5 protein
;Species: phage T3
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text
C;Accession: S07506
R;Beck, P.J.; Gonzalez, S.; Ward, C.L.; Molineux, I.J.
J. Mol. Biol. 210, 687-701, 1989
A;Title: Sequence of bacteriophage T3 DNA from gene 2.5
A;Reference number: S07500; MUID:90133923; PMID:2614843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                               N;Alternate names: T7 lysozyme
C;Species: phage T7
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981
C;Accession: C94615; D92866; S42302; S43502; A01001
                                                                                                                                      RESULT
MUBPA7
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N-acetylmuramoyl-L-alanine amidase (EC
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R;Dunn, J.J.; Thompson, K. submitted to the Nucleic A A;Reference number: A94615
                                                                                                 N-acetylmuramoyl-L-alanine amidase N; Alternate names: T7 lysozyme
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C;Genetics:
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A; Residues: 1-151 <BEC>
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                                                                                                                                                                                                       KGKFDANFTPAQMQSLRSLLVTLLAK--
                                                                                                                                                                                                                                     RVP----TPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQL
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   A94615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: X17255; NID: g15682;
               Acid Sequence
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                            Mismatches
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hes 82;
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Wait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID: 21016719; PMID: 11130712
                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: F96558
R; Theologis, A.; Ecker, J.R.; Palm,
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C;Keywords: hydrolase
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A; Molecule type: DNA
A; Residues: 1-38, 'E', 40-118, 'V', 120-151 <DUW>
A; Residues: 1-38, 'E', 40-118, 'V', 120-151 <DUW>
A; Cross-references: EMBL: V01146; NID: 9431187; PIDN: CAA24403.1; PID: 943
C; Comment: This late gene protein is not required for lysis but plays
Lly bound. The functional significance of this is not clear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Dunn, J.J.; Studier, F.W. submitted to the EMBL Data Library,
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J. Mol. Biol. 166, 477-535, 1983

A;Title: Complete nucleotide sequence of bacteriophage 'A;Reference number: $42283; MUID:83241725; PMID:6864790
A; Map
                                                                                        A; Molecule type: DNA
A; Residues: 1-879 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
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C; Superfamily: phage T7 N-acetylmuramoyl-L-alanine amidase
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A;Residues: 1-38,'E',40-151
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                                             Genetics:
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position:
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                                                                                                                                      preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVP-----TPQAIRAAQGLLACGVA--QGALRSNYVLKGHRDVQRTLSPGNQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGKFDANFTPAQMQSLRSLLVTLLAKYEGA-----GLRAHHEVAPKACPSFDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REIROWH-KDQGWLDVGYHFIIKRDGTVEAGRDEMAVGSHAKG-YNHNSIGVCLVGGIDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S42302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                GB:AE005173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                NID: g9802791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 120; DB 1;
Pred. No. 0.00029;
                                                                                                                                                                                                                                                                                                                                                                                                               C.J.; Federspiel, N.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                October 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                PIDN: AAF99860.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 151;
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                                                                                                                                                                                                                                               A.M.; Sun,
                                                                                                                                                                                                                                                                                               Maiti,
                                                                                                                                                                                                                                                                                                                    Khaykin,
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                                                                                                                                                                                                                                                                                                                                                                                          Т.Н.;
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                                                                                                                                                                                                                                                                                                                       Kim,
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Query

Match

8.78;

Score

91; DB

2

Length 879;

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A; Variety:
C; Date: 12-
                                                                                                                                                                                                                                          C;Date: 12 Feb-1999 #sequence_revision 12-Feb-1999 #text_change 29-Sep-1999 C;Accession: H71878
C;Accession: H71878
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; V. Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                    stationary phase protein - Helicobacter pylori (strain
C; Species: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽
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A; Residues: 1-268 <W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                            A;Title: Genomic sequence comparison of two unrelated isolates A;Reference number: A71800; MUID:99120557; PMID:9923682 A;Accession: H71878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: Z19883
A; Accession: T24371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T02G6.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                                                                                                           A; Cross-references: GB: AE001516; A; Experimental source: strain J99
                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-267 <ARN>
                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; McLay,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Cross-references: EMBL:Z81583; PIDN:CAB04668.1; GSPDB:GN00019; CESP:T02G6;Experimental source: clone T02G6
                                                       Superfamily: stationary-phase survival protein SurE
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Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNNTNNKCPSDPLDLFPMKMESPLINFLDFKYN-----ITFDGEIWNFKYNCRFIQTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCNTPASCQQQARNVQHYHMKT---LGWCDVGYNFLIGEDGLVYEGRGWNF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MMVAWGRPTF - - - -
                                                                                                                                                                                                                                                                                                                                     strain J99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32; Conserv
       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---TGAHSGHLWNPMSIGISFMGNYMDRVPTPQ
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20.3%;
     7.6%;
26.1%;
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                                                                                                                           GB:AE001439;
     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 82; [
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.4,
); Mismatches
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     79.5;
No. 4.
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DB
4.5;
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                                                                                                                           NID: g4155431; PIDN: AAD06448.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138
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                                                                                                                                                                                                                               the human
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                                                                                                                                                                                                                              gastric
                                                                                                                                                                                                                                                                                Smith,
                                                                                                                           PID:g41554
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                                                                                                                                                                                                                                                                G.F.;
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RESULT 9
C85087
                                                                    A; Gene
A; Map
                                                                                                                                                                                                                                                                                                                             hypothetical protein AT4908700 [imported] - Arabidopsis thaliana c;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C;Accession: C85087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, I Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McK. Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Avauture 388, 539-547, 1997

Avauthors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fras A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A; Reference number: A64520; MUID:97394467; PMID:9252185

A; Accession: B64636
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                                                                                                                                                                                                                    A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Reference number: A85001; MUID:20083488; PMID:10617198 A;Accession: C85087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                닭
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C;Date: 09-Aug-1997 #sequence_
                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-432 <STO>
                                                                                                                                                                                                                                                                                  R; anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
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A; Residues: 1-267 < TOM>
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                                                                                                                                  A;Cross-references:
Query Match
Best Local Similarity
                                                                                                             Genetics:
                                                                                                                                                                                                  Status: preliminary
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Best Local
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                                                                                      AT4908700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INELFKHYCFDLVISGINLGSN--MGED-TIYSG---TVAGAIEGTIQGVPSIAISQILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNVQHYHM----KTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNPMSIGISFMGN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QALEEMAETYVVAPKHE-KSACSQCIT-TTAPLRAEKIKGKEGRHYRIDDGTPSDCVYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHTAGS----SCNTPASCQQQA 72
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                                                                                                                                  GB:NC_001268;
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  7.4%;
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    Score
Pred.
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Pred. No. 4
                                                                                                                                  NID: g7267512; PIDN: CAB77995.1;
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    78;
No.
DB
11;
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                         Length
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A;Gene: MAC25
C;Superfamily: Kazal proteinase inhibitor homology
F;104-156/Domain: Kazal proteinase inhibitor homol
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()Species: Homo sapiens (man)
()Species: Homo sapiens (man)
()C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
(;Accession: I52825
(;Accession: I52825
R;Murphy, M.; Pykett, M.J.; Harnish, P.; Zang, K.D.; George, D.L.
(cell Growth Differ. 4, 715-722, 1993
(cell Growth Differ. 4, 715-722, 1993)
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
S50031
                                                                                                                                                                                                                                         Biochem. J. 303, 591-598, 1994
A;Title: Purification and molecular cloning of prostacyclin-stimulating factor A;Reference number: S50031; MUID:95071263; PMID:7980422
A;Accession: S50031
                                                                                                                                                                                                                                                                                                                                             prostacyclin-stimulating factor C;Species: Homo sapiens (man) C;Date: 01-Aug-1995 #sequence_revi C;Accession: S50031
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C; Genetics:
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A;Molecule type: mRNA
A;Residues: 1-277 <RES>
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                            Q
                                                                                                                                 C; Superfamily: Nazar pro
F; 104-156/Domain: Kazal
                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-282 < YAM>
                                                                                                                                                                                                                                                                                                           R; Yamauchi, T.; Umeda, F.; Masakado, M.; Isaji, M.; Mizushima, S.; Biochem. J. 303, 591-598, 1994
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                                                                   Query Match
Best Local S
Matches 49
                                                                                                                                                          Cross-references: GB:S75725; NID:g861520; PIDN:AAB32370.1; PID:g861521; Superfamily: Kazal proteinase inhibitor homology
                                                                                                                                                                                                                                                                                                                                                            Species: Homo sapiens (man)
Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 28-May-1999
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGGPGVSGVCVCKSRYPV----CGSDGTTYPSGCQLRAASQRAESRGEKAITQVSKGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSLLRLGA-AQETEDPACCSPIVPRNE------WKALASECAQHLS-----
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PPLPPLGCLLGETRDACGCCPMCARGEGEPCGGGGAGRGYCAPGMECVKSRKRRKGKAGA 100
                                 PSLLRIGA-AQETEDPACCSPIVPRNE-----
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                                                                                        Similarity
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                                                                     Conservative
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                                                                                                                                             proteinase inhibitor homology
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23.1%;
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Pred. No. 7
                                                                                      Score 77.5; DI
Pred. No. 7.4;
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                                 -WKALASECAQHLS-----
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RESULT 13
D65096
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Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: D65096
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submitted to the Protein
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                                                                                                                                                                                                                                                                                                                                      hypothetical 40.1 kD protein in ebgC-exuT intergenic C;Species: Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AL138648
A;Experimental source: cultivar Columbia;
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                                                                                                           A;Cross-references: GB:AE000390; GB:U00096; NID:g2367189; A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-356 <BLAT>
                                                                                                                                                                                                                                                                                                     C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source:
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A; Accession: T48111
                                                                                                         A; Experimental source:
                                                                                                                                                                          A;Status: preliminary; nucleic acid
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;Species: Arabidopsis thaliana (mouse-ear cress)
;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
;Accession: T48111
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Matches 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YMDRVPTPQA-IRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLY
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Sequence Database, April 2000
                   7.48;
21.38;
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     17;
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Pred. No. 9.4;
29; Mismatches
Score 77.5; DI
Pred. No. 9.8;
17; Mismatches
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                                                                                                                                                                                                                                                                                   C.A.; Perna, N.T.; Burland, V.;
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                                                                                                                                                                                                                                K-12
                                                                                                                           PIDN: AAC76114.1;
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DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: A98124
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                                        C;Accession: H85968

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: H85968
                                                                                                                                                                                                             hypothetical protein ygjJ [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli C;Date: 16-Teb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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A;Residues: 1-356 <HAY>
A;Residues: 1-356 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37384.1; PID:913363434; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein ECs3961 [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli
C;Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
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A; Status: preliminary
A: Molecule type: DNA
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Best Local Similarity 21.3
Matches 46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KALASECAQHLSLPLRYYVVSHTAGSSC-----NTPASCQQQARNVQHYHMKTLGWC 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLITAPCRALLALPFCYAF -- SAAGEEARPAEHDDTKTPAITSTSSPSFRFYGELGVG -- 57
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21.3%; Pred. No. 9.8;
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A;Residues: 1-356 <STO>
A;Cross-references: GB:AE005174; NID:g12517663; PIDN:AAG58212.1; GSPDB:GN00145; UWGP:A;Experimental source: strain O157:H7, substrain EDL933
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DIMTALKVONLSGNFRYSVTATPAGHHDESKAWLHF 202
                                      DVQRTLS----PGNQLYHLI------QNWPHY 188
                                                                           GFEGGINRFYGGYRTNDGTEIMLSLRQ------DSSLDDLQWWGDFTPDLGYVIPNTR 166
                                                                                                               PMSIGIS-FMGNYMDRVPTPQAIRAAQGLLACGVAQGALRS-----NYVLKGHR 166
                                                                                                                                                                                             DVGYNFLIGED-----HLWN 118
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Pred. No. 9.8;
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Search completed: November 12, 2002; 02:28:05 Job time: 83 secs

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Maximum DB seq length: 2000000000
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DNA encoding prote
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ALIGNMENTS

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RESULT 1 AAX21820 ID AAX2 XX AC AAX2 XX Human tag7 clone coding sequence. AAX21820; AAX21820 standard; cDNA to mRNA; 718 18-MAY-1999 (first entry)

Tag7; tumour growth inhibitor; mammalian tumour; carcinoma; sarcoma; melanoma; leukaemia; apoptosis inducer; human; ss.

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New nucleic acid encoding tag7 - used to inhibit tumour growth and induce apoptosis, for treatment of carcinoma, sarcoma, melanoma and
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P-PSDB; AAY00771.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an antibody that binds to a human CC protein (I) selected from: pro381; pro1269; pro1410; pro1755; pro1780; CC pro4344; pro1927; pro15567; pro1295; pro1293; pro4334; pro4354; pro4359; pro1555; pro1096; pro2038; and pro2262. (I) has CC anticancer activity and can be used to diagnose tumours in mammals, by CC detecting complex formation when the antibody is contacted with test CC cells. Increased expression of genes encoding (I) can also be detected CC diagnose tumours. Agents which inhibit the activity of (I), can be used to diagnose tumours growth, CC especially the antibodies, or an antisense oligonucleotide which CC preferably by inducing cell death. Methods from the present invention CC can be used to identify compounds which inhibit the biological activity CC of (I). AAC58019 to AAC58102 represent invention for human PRO CC sequences. AAC58103 to AAC5812 and AAB24021 to AAR24404 prepresent human PRO CC probes used in examples from the present invention for human PRO CC promotes and protein sequences given in the examplification of CC the present invention.
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01-DEC-1999;
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the growth of tumors in
polypeptide activity or
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TyrGluGlyArgGlyTrpAsnPheThrGlyAlaHisSerGlyHisLeuTrpAsnProMet
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                                                                                                                          AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA3730 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
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                                                                                                                                        GGCAACTACATGGATCGGGTGCCCACACCCCAGGGCCATCCGGGCAGCCCAGGGTCTACTG
                                                                                                                                                                                                                                                                                                                  CCCTTACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGGCTCG
                                                                                                                                                                                                                       GTGGGCTACAACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAAC
                                                                                                                                                                                                                                    GTGGGCTACAACTTCCTGATTGGAGAAGACGGGCTCGTATACGAAGGCCGTGGCTGGAAC
                                                                                                                                                                                                                                                                     TGCCAGCAGCAGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 680;
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Paoni NF, Roy MA,
be CK, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            697 BP; 136 A; 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Botstein D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acids may also be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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owski PJ, Grimaldi CJ,
MA, Smith V, Stewart TA
PM, Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 674;
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TA, Tumas D;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                          immune disorder; Addison's disease; rheumatoid arthritis; dern multiple sclerosis; inflammatory disorder; inflammatory bowel crohn's disease; nephritis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myocarditi
                                                                                                                                                                                                                                                                                                                                                                                                         melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                         antirheumatic, dermatological; antiproliferative; antiarteriosclerotic;
anticancer; vulnerary; antiviral; antibacterial; antifungal;
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted protein; immunosuppressant; anti-inflammatory; antiarthritic; antirheumatic, dermatological; antiproliferative; antiarteriosojerotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Htag7
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                                                                                                                                                                                                                                                                                                                                                                                                    wound healing; human; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                           disease;
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Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer wounds, and infectious diseases -P-PSDB; AAB25583 Greene Ni J, 28-OCT-1998; 27-OCT-1999; 25-MAY-2000 W0200029435-A1 (HUMA-) HUMAN 2000-387742/33. SM, GENOME SCI INC 98US-0105971 99WO-US25031 Olsen HS, Young PE, Kenny JJ, Moore PA, Wei cancer

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Claim 1; Figure

34; 803pp; English.

CC nucleotide sequences encoding them. The polynucleotide sequences given in AAA80606-A80623 encode the 12 secreted protein sequences given in CC AAB25576-B2559. The human secreted proteins have various activities of the proteins in which they are expressed. Examples of the CC antivities of the proteins include: immunosuppressant; CC antivities antibacterial; antiarteriosclerotic; anticancer; vulnerary; CC antivital; antibacterial; and antifungal activity. The proteins, CC antivital; antibacterial; and antifungal activity. The proteins, CC and/or diagnose various disease, disorders and conditions examples of arthritis, dermatitis, and multiple sclerosis; inflammatory disorders e.g. Addison's disease, rheumatoid CC e.g. inflammatory bowel disease, Crohn's disease and nephritis; CC ardiovascular disorders e.g. coronary arteriosclerosis and protein genes infectious diseases. The human secreted protein gene #8 and protein genes are represented in sequences AAA80613 and AAB25583. Sequences xx AAA80662-A80663 represent genes related to the secreted protein gene#8. The present invention relates to 12 secreted human proteins and to nucleotide sequences encoding them. The polynucleotide sequences

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                                                                                Peptidoglycan recognition protein-like protein; PGRP; PGRP-C; reg chondrosarcoma; immunosuppressive; antibacterial; anti-apoptotic; tumour necrosis factor; TNF; anti-infectious; mononuclear phagocy inhibitor; protein co-ordinate data; ss.
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3.7e-161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human peptidoglycan recognition protein-like proteins (PGRP) expressed by keratinocytes (PGRP-K), wound healing tissues (PGRP-W) or chondrosarcoma tissue (PGRP-K), wound healing tissues (PGRP-W) or chondrosarcoma tissue (PGRP-K) are disclosed. The PGRP DNA and proteins are useful for preventing, treating or ameliorating a medical condition in a mammal (claimed). PGRP is useful in augmenting the immune system in such areas as immune recognition, antipen presentation and immune system activation. Antibodies or antagonists directed against these proteins may be useful in-reducing or eliminating disorders associated with tumour necrosis factor (TMF) and TMF-like Cytokines, such as endotoxic shock and autoimmune disorders and for treating infectious diseases including silicosis, sarcoidosis and idiopathic contents of the protein such as the contents of the contents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide encoding peptidoglycan recognition protein-like antibodies specific to it useful for preventing, treating condies; endotoxic shock and auto-immune disorders and infections i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-2000
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                                                         TGGGCTACAACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACT
                                                                                                                                                                                                  CCTTACGCTATGTGGTGGTATCGCACACGCCGCCAGCAGCAGCTGCAACACCCCCCGCCTCGT
TCACGGGTGCCCACTCAGGTCACTTATGGAACCCCCATGTCCATTGGCATCAGCTTCATGG
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55..117
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118..642
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Pred. No. 3.7e-161;
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Best Local S
Matches 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes the human tag? of the invention. Cells containing the tag? DNA sequence are used to express recombinant tag? Tag? is used to produce and purify antibodies; to inhibit growth of mammalian tumours, especially for treating carcinoma (of liver, ovary, breast, cervix, lung, prostate, colon/rectum, bladder, testis, stomach, pancreas, mouth, head and neck, squamous cell carcinoma or teratocarcinoma), sarcoma (Kaposi's, osteo- or fibro-sarcomas), melanoma or leukaemia; and as a molecular weight marker. The tag? polypeptide inhibits tumour growth and induces appotosis. The tag? polypeptide inhibits tumour growth and sprobes for gene mapping and detection of tag? gene expression, and as primers. Antibodies against tag? are used as reagents for detecting tag?; as an antagonist of tag?; for isolating tag? and therapeutically to inhibit or delay tumour materartaries.
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CCGCTCTATGCTGCTTGCCTGGGCTCTCCCCAGCCTCCTTCGACTCGGAGCGGCTCAGGA 120
                                                                                                        CAACTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTCTCCAGGCAACCAGCT
                                                                                                                     CAACTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTCTCCCAGGCAACCAGCT
                                                                                                                                                                             GGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCTCAGGGAGCCCTGAGGTC
                                                                                                                                                                                                                               CCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGGATCGGGTGCCCACACCCCA 480
                                                                                                                                                                                                                                                                                                                           CCACATGAAGACACTGGGCTGGTGCGACGTGGGCTACAACTTCCTGATTGGAGAAGACGG
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                         CCCCATTCCTCCCCTCCCATGGCCAAAAACCCCCACTGTCTCCTCTCCCAATAAAGATG
                                                                                                                                                                                                                  CCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGGATCGGGTGCCCACACCCCA
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                                                                                                                                                               GGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCTCAGGGAGCCCTGAGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 126-127; 138pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 142
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Pred. No. 1.4e-172;
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                                                                                                                                                                                                                                                                                                                           The present invention describes an antibody that binds to a human CD protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO4344; PRO1927; PRO1557; PRO1293; PRO1303; PRO1303; PRO4344; PRO4354; PRO4397; PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262 (I) has anticancer activity and can be used to diagnose tumours in mammals, by detecting complex formation when the antibody is contacted with test cells. Increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), especially the antibodies, or an antisense oligonucleotide which hybridises to genes encoding (I), can be used to inhibit tumour growth, preferably by inducing cell death. Methods from the present invention can be used to identify compounds which inhibit the biological activity of (I). AAC58019 to AAC58102 represent PCR primers and hybridisation probes used in examples from the present invention for human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                   Query Match
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Matches 680
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01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
01-DEC-1999;
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                                                                                                                                  29
                                                                                  N
CCCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCC 148
                                                                                                                          CCTGGACATGTACCTGCAGCCACTATGTCCCGCCGCTCTATGCTGCCTTGCCTGGGCTCTC
                                                                          2000-594320/56.
DB; AAB24022.
                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                   BP; 136
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99WO-US20111.
99US-0162506.
99WO-US28313.
99WO-US28634.
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Pred. No. 2e-161;
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                                                                                                                                                                                                                                DB 21;
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                                                                                                                                                                                            AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO porteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA3730 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                            New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
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                                                                                                                                                                                                                                                                             DNA encoding protein of the invention
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    This cDNA sequence encodes the claimed antimicrobial peptide f
                                                                Claim 13; Fig 4; 56pp; English.
                                                                                                                 Antimicrobial (poly)peptide(s) from bovine and murine granulocytes useful therapeutically, as preservatives for food, in water treatment and in agriculture
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DB; AAW23722.
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560..598
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precursor (see AAW23722) of a from bovine neutrophils, design
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bovine granulocyte peptide A or BGP-A (see AAW23724). It was isolated from bovine bone marrow cDNA using PCR and RACE procedures. The encoded HGP-A precursor comprises a 21-amino signal peptide, a 156-residue propeptide and 13 C-terminal am acids corresponding to mature BGP-A. BGP-A and the murine
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TAAAG 672
                        TAAAG 715
                                                                                                                                                          ACCTGACTCCTAACTACGAAGTCAAAGGACACCGCGATGTGCAGCAGACGCTCTCTCCAG
                                                      TCCGTCTTC
                                                                 CTGATCCGCACCCCATTCCTCCCCTCCCATGGCCAAAAACCCCACTGTCTCCCTTCTCCCAA
                                                                                                   GGGACGAGCTCTATAAAATCATCCAGCAGTGGCCGCACTACCGCCGCGTGTGAGGGCCTG
                                                                                                                      GCAACCAGCTCTACCACATCCAGAATTGGCCACACTACCGCTCCCCCTGAGGCCCTG
                                                                                                                                                                            CCCTGAGGTCCAACTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTCCCAG
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                                                                                                                                                                                                                                        CCACACCCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCTCAGGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCCATAGTGCCCCCGGAACGAGTGGA 170
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                                             -TCACACCCCACCCATCCCATCAGAAACCCCACCGCCTTCCCCTGCCCCAA
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72.98;
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Pred. No. 4.5e-79;
0; Mismatches 161
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                                                                                                                                                                                                                                                                                                                      sequences, corresponding to human secreted proteins. AALONG AAX65438 represent the EST-related proteins corresponding to AALA2265 to AAX43052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, as well as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in diagnostic procedures to identify individuals, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal gene expression. The products may also be used in gene therapy protocols. The nucleic acids encoding signal peptides can be used for directing extracellular secretion of a polypeptide or the
                                                                                                                                                                                                               Sequence 380 BP; 67 A; 130 C; 114 G;
                                                                                                                                                                                                                                                        insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins is valuable. AAZ42249 to AAZ42264 and AAX64644 to AAX64650 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel
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28-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; chromosome mapping; upstream regulatory sequence;
forensic; location; development; protein synthesis; stability;
regulation; identification; ss.
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                                                                                                                                                                   Local Similarity
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                                                                                                        GGGCCCCTGGACATGTACCTGCAGCCACTATGTCCCGGCCGCTCTATGCTGCTTGCCTGGG
 GCCCCATAGTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCCAGCACCTGA
                              CTCTCCCCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCCGGCCTGCTGCA 143
                                                                                          GGTCTCCCGGCCCTGCCCCTGCCACTATGTCCCGCCGCTCTATGCTGCCTTGCCTGGG
                                                                                                                                                    358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secreted protein 5' expressed ostic, forensic, gene therapy,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to AAZ43075 represent novel 5' expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 336; 837pp; English.
                                                                                                                                                                                                                                             used
                                                                                                                                                    Conservative
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98US-0069047
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95.08;
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No. 2.6
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                                                                                                                                                                 2.6e-77
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                                     This sequence encodes the murine tag7 of the invention. Cells containing the tag7 DNA sequence are used to express recombinant tag7. Tag7 is used to produce and purify antibodies; to inhibit growth of mammalian tumours, especially for treating carcinoma (of liver, ovary, breast, cervix, lung, prostate, colon/rectum, bladder, testis, stomach, pancreas, mouth, head and neck, squamous cell carcinoma or teratocarcinoma), sarcoma (Kaposi's, osteo- or fibro-sarcomas), melanoma or leukaemia; and as a molecular weight marker. The tag7 polypeptide inhibits tumour growth and induces apoptosis. The tag7 coding sequences are also useful as probes for gene mapping and detection of tag7 gene expression, and as primers. Antibodies against tag7 are used as reagents for detecting tag7; as an antagonist of tag7; for isolating tag7 and therapeutically to inhibit or delay tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tag7;
                                                                                                                                                                                                                                               Claim 3; Fig 1; 138pp; English.
                                                                                                                                                                                                                                                                                           New nucleic acid encoding tag7 - used to inhibit tumour growth and induce apoptosis, for treatment of carcinoma, sarcoma, melanoma and
                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-120887/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse tag7 clone coding sequence.
                                                                                                                                                                                                                                                                               leukaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour growth inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mammalian tumour; carcinoma; sarcoma;
inducer; mouse; ds.
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Query Match Best Local Similarity

Score Pred.

316.6; DB 20; NO. 8.8e-71;

Length

Sequence 549

B₽;

117

A; 161 C; 44.18; 77.28;

151 G; 120

T; 0 other;

granulocytes water

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RESULT 10
AAT78510
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                                                                                                                                                                                                                                                                       Antimicrobial peptide; antibiotic; antibacterial; antifungal; fungicide; antiprotozoa; protozoacide; antiviral; virucide; murine granulocyte peptide A; MGP-A; preservative; sepsis; endotoxaemia; mouse; ss.
(REGC ) UNIV
                           16-FEB-1996;
                                                      13-FEB-1997;
                                                                                 21-AUG-1997.
                                                                                                            WO9729765-A1
                                                                                                                                                                mat_peptide
                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                         Murine granulocyte peptide A precursor cDNA.
                                                                                                                                                                                                                                                                                                                                                                         18-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                           96US-0011834
                                                      97WO-US02218
                                                                                                                                    /#tag= b
/product=
                                                                                                                                                               /transl_except= 543..578
                                                                                                                                                                                                     Location/Qualifiers 36..581
                                                                                                                                               /*tag=
                                                                                                                                                                                       /*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC This CDNA sequence encodes the precursor (see AAW23723) of a novel, claimed antimicrobial peptide from bovine neutrophils, designated CC murine granulocyte peptide A or MGP-A (see AAW23725). It was considered from murine bone marrow cDNA using primers based on the MGP-A cDNA (see AAW23725). It was considered from murine bone marrow cDNA using primers based on the MGP-A cDNA (see AAW23725). The considered MGP-A precursor CC comprises signal peptide and propeptide sequences followed by 12 creminal amino acids corresponding to mature MGP-A. MGP-A and GGP-A (see AAW23724), exhibit activity against Gram-positive and GGP-A (see AAW23724), exhibit activity against Gram-positive and CC BGP-A (see AAW23724), exhibit activity against Gram-positive and CC Exam-negative bacteria, fungi and viruses, specifically staphylococcus aureus, Escherichia coli, Candida albicans, CC salmonella typhimurium and C. neoformans (claimed). They can be used in human or veterinary medicine (particularly to treat claimed) or as preservatives in food products or in water cupiles (claimed). They can also be applied to crops to reduce post-harvest spoilage or expressed in transgenic plants to increase their disease resistance. They have low immunogenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 677
                      556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment and in agriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antimicrobial (poly)peptide(s) from bovine and murine useful therapeutically, as preservatives for food, in
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                     AAAGCTGCGAACACTACCG
                                                                                                                          CCCTANATCTTCTGGAATCTGGGGTGTCTCGGGGGCTTCCTGAGATCCAACTATGAAGTCA
                                                                                                                                        CCCAGGGTCTACTGGCCTGCGGTGTGGCTCAGGGAGCCCTGAGGTCCAACTATGTGCTCA
                                                                                                                                                                              GCATCACCTTCATGGGGAACTTCATGGACCGGGTACGCAAAGC---GGCCCTCCGTGCTG
                                              AGAATTGGCCACACTACCG
                                                                  AAGGACACCGGGATGTGCAAAGCACTCTCTCTCCAGGTGACCAACTCTATCAGGTCATCC
                                                                                  AAGGACACCGGGATGTGCAGCGTACACTCTCTCCAGGCAACCAGCTCTACCACCTCATCC
                                                                                                                                                                                                 GCATCAGCTTCATGGGCAACTACATGGATCGGGTGCCCACACCCCCAGGCCATCCGGGCAG
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DB; AAW23723.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 146 A; 217 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.98;
76.68;
                   574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.10); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 300.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 G; 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.1e-66;
ches 114;
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677; ω

Gaps

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614 495

555

494

554 435 434 318

258 314

378

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                                                                                                                                                                                   nucleotide sequences encoding them. The polynucleotide sequences given in AAA8606-A80623 encode the 12 secreted protein sequences given in AAA86066-A80623 encode the 12 secreted protein sequences given in AAA86066-A80623 encode the 12 secreted protein sequences given in AAA86066-A80623 encode the 12 secreted protein sequences given in CAAB25576-B2593. The human secreted protein shave various activities of the proteins include: immunosuppressant; antipiniferative; antiarteriosclerotic; anticancer; vulnerary; cantiproliferative; antiarteriosclerotic; anticancer; vulnerary; cantiviral; antibacterial; and antifungal activity. The proteins, conditions examples of the polyperides, agonists and antigonists may be used to treat prevent and/or diagnose various disease, disorders and conditions examples of which include: immune disorders e.g. Addison's disease, rheumatoid arthritis, dermatitis, and multiple sclerosis; inflammatory disorders e.g. faddison's disease and nephritis; cardiovascular disorders such as paraproteinaemias and purpura; cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The proteins and polynucleotide infertions disease in the human scorotid arthritis that the teatment of the factors and a sequences may also be used in wound healing and the treatment of
                                                                 Query Match
Best Local
                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecules encoding human secreted proteins a used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Greene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crohn's disease, nephritis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antirheumatic,
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                ACCCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCTCAGGGAGCCCT
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1 Similarity
242; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ncer; vulnerary; antiviral; antibacterial; antifunga. disorder; Addison's disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lymphoma;
                                                                                                                                                       diseases. The human secreted protein gene #8 and protein are represented in sequences AAA80613 and AAB25583. Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infectious diseases
                                                  Conservative
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                                                                                                             BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in; immunosuppressant; anti-inflammatory; antiarthritic;
dermatological; antiproliferative; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0105971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein gene #8 related gene HBMTB79R SEQ
                                                                                                                                            represent genes
                                                                                                               71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              757;
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                                                                                                             ð,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory disorder; inflammatory bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                 32.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             relates
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                                                                                                               99
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                                                0;
                                                            Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             12 secreted human proteins and m. The polynucleotide sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kenny JJ,
                                                                                DB
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                                                                                                               other,
                                                                                                                                            the secreted
                                                                              Length 285;
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RESULT 12
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dependent on the tissues in which they are expressed. Examples o activities of the proteins include: immunosuppressant; anti-inflammatory; antiarthritic; antirheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; and antifungal activity. The proteins, polypeptides, agonists and antagonists may be used to treat prevently of the proteins of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antirheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antifungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
                                                                                                                                                                    nucleotide sequences encoding them. The polynucleotide sequences given in AA80606-A80623 encode the 12 secreted protein sequences given in AA825576-B25593. The human secreted proteins have various activities
                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crohn's disease; nephritis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ni J,
                                                                                                                                                                                                                                                          The present invention relates to
                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Secreted protein; immunosuppressant; anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-OCT-1999;
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infectious diseases -
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healing; human; ss.
                                                                                                                                                                                                                                                                                                         803pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Young
                                                                                                                                                                                            to 12 secreted human proteins and the them. The polynucleotide sequences given 12 secreted protein sequences given in
                                                                                                                                                                                                                                                                                                            English.
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                                                                                                     Venter
                                                                                                                                                                                         23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                WO200171042-A2
                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
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                                                                                                                                             (PEKE ) PE CORP NY.
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2000US-0614150
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    detection
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Best Local
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                                            3786
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                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                       insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical;
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                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
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AGACACTGGGCTGGGGCTGGGCTACAACTTCCTGATTGGAGAAGACGGCCTCGTAT
                                                                                                  GGACCGTAGGCCTGGGCAACTACCTCAGCTACGCCATCATCCACCACACCGCCGGCTCCT
                                                                                                                            GCGCCCAGCAGCTGAGCCTTGCCCTTACGCTATGTGGTGGTATCGCACACGGCGGCCAGCA 248
                                                                                                                                                          ACATGGCCCAGGGCGTCTATGTCGTCTCCAAGGCGGAGTGGGGGTGGTCGCGGCGCCAAAT
                                          ACTGCGAGACCCCGTGCCCAGTGCAACGCCCGTGCTGCAGAGCGTCCAGAACTACCACATGG
                                                                      GCTGCAACACCCCCGCCTCGTGCCAGCAGCAGCCCGGAATGTGCAGCACTACCACATGA 308
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 29101; 21pp + Sequence Listing;
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2000US-0614150
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Pred. No. 1.2e
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                                                                                                                                                    3726 ACTCCCTGGGCTGGCCCGACATCGGCTACAACTTCCTGATCGGCGGAGACGGCAACGTGT 3667
                                                 609 TCATCCAGAATTGGCCACACT 629
                                                                                                                           489 GGCAGCCCAGGTCTACTGGCCTGCGGTGTGGCTCAGGGAGCCCTGAGGTCCAACTATG 548
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-MODEL-frame+_p2n.model -DEV=xlp
-Q-/c9n2_1/USP70_spool/US99462625/runat_07112002_101525_24830/app_query.fasta_1.327
-Q-/c9n2_1/USP70_spool/US99462625/runat_07112002_101525_24830/app_query.fasta_1.327
-DB=N_Geneseq_101002 _OPMT-fastap -SUFFIX=rng -MINMARCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=-buman40.cd1
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT-pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09462625_@CGCN_1_1_281_ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US09462625_@CGCN_1_1_281_ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US09462625_@CGCN_1_1_281_ext -HEAPSIZE=7 -1001525_24830 -NCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1051
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SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*

SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*

SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

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Copyright (c) 1993 - 2002 Compugen Ltd.
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
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SUMMARIES

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ALIGNMENTS

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14-SEP-2000.		WO200053750-A1.		Homo sapiens.		fication;	Human; tumour; diagnosis; neoplast	ı	Human PRO1269 nucleotide sequence		25-JAN-2001 (first entry)		AAC58104;		AAC58104 standard; cDNA; 697 BP.	AAC58104	RESULT 1

Human; tumour; diagnosis; neoplastic disease; proliferation; cancer; identification; tumourigenesis; anticancer; detection; ss.

Human PRO1269 nucleotide sequence SEQ ID NO:6.

WO200053750-A1

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                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC The present invention describes an antibody that binds to a human protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; CC PRO3434; PRO1927; PRO3567; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397; PRO1557; PRO1555; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397; PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has certainly complex formation when the antibody is contacted with test (Cc lis. increased expression of genes encoding (I) can also be detected to diagnose tumours. Agents which inhibit the activity of (I), and cespecially the antibodies, or an antisense oligonucleotide which (CC expecially the antibodies, or an antisense oligonucleotide which (CC expecially by inducing cell death. Methods from the present invention (CC can be used to identify compounds which inhibit the biological activity (CC of (I). AAC58019 to AAC58102 represent PCR primers and hybridisation (CC probes used in examples from the present invention for human PRO (CC sequences. AAC58103 to AAC58122 and AAB24021 to AAB24040 represent human (CC proposed) invention and protein sequences given in the exemplification of the present invention for human processors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAR-1999;
01-SEP-1999;
29-OCT-1999;
30-NOV-1999;
01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibodies specific for PRO polypep the growth of tumors in mammals, an polypeptide activity or expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 50; Fig 3;
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                                                                                                                                                                                                                                                        present invention.
                                                                                                                                         2000-594320/56.
                                                                                  AspProAlaCysCysSerProIleValProArgAsnGluTrpLysAlaLeuAlaSerGlu 40
TyrGluGlyArgGlyTrpAsnPheThrGlyAlaHisSerGlyHisLeuTrpAsnProMet
                                         LysThrLeuGlyTrpCysAspValGlyTyrAsnPheLeuIleGlyGluAspGlyLeuVal 100
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99WO-US20111.
99US-0162506.
99WO-US28313.
99WO-US28634.
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screening;
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                                                                                                                                                                                                                                                                               AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA3730 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 200
P-PSDB;
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                 The present invention relates to secreted and transmembrane proteins. These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. They may also be used used to generate either transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents.
                                                                                                                                                                                                                                                                                                       WPI;
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Paoni NF, Roy MA, S
Pe CK, Williams PM, W
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1 PJ, Grimaldi CJ, GI
Smith V, Stewart TA,
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10-JUL-1998;
                                           Homo sapiens
                                                        Tag7; tumour growth inhibitor;
melanoma; leukaemia; apoptosis
                                                                               Human tag7
                                                                                             18-MAY-1999
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              21-JAN-1999
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LysThrLeuGlyTrpCysAspValGlyTyrAsnPheLeuIleGlyGluAspGlyLeuVal 100
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The present invention relates to 12 secreted human proteins and the CC nucleotide sequences encoding them. The polynucleotide sequences given in Nab86066-80623 encode the 12 secreted protein sequences given in CC AAB25576-B25593. The human secreted proteins have various activities CC dependent on the tissues in which they are expressed. Examples of the CC activities of the proteins include: immunosuppressant:
CC anti-inflammatory; antiarthritic; antirheumatic, dermatological;
CC antiproliferative; antiarteriosclerotic; anticancer; vulnerary;
CC antivital; antibacterial; and antifungal activity. The proteins,
CC polypeptides, agonists and antagonists may be used to treat prevent
CC and/or diagnose various disease, disorders and conditions examples of which include: immune disorders e.g. Addison's disease, rheumatoid
CC arthritis, dermatitis, and multiple sclerosis; inflammatory disorders (e.g. inflammatory bowel disease, Crohn's disease and nephritis;
CC cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis;
CC cancer e.g. melanoma and lymphoma. The protein and polynucleotide sequences may also be used in wound healing and the treatment of infectious diseases. The human secreted protein gene #8 and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crohn's disease; nephritis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Figure 34; 803pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acid molecules encoding human secreted proteins a used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, can
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                                                                                                    Peptidoglycan recognition protein-like protein; PGRP; PGRP-C; regula chondrosarcoma; immunosuppressive; antibacterial; anti-apoptotic; tumour necrosis factor; TNF; anti-infectious; mononuclear phagocyte; inhibitor; protein co-ordinate data; ss.
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                                                                                                                                                                                                                                                                                                                                                                  Novel human peptidoglycan recognition protein-like proteins (PGRP) expressed by keratinocytes (PGRP-K), wound healing tissues (PGRP-W) or chondrosarcoma tissue (PGRP-C) are disclosed. The PGRP DNA and proteins are useful for preventing, treating or ameliorating a medical condition in a mammal (claimed). PGRP is useful in augmenting the immune system in such areas as immune recognition, antigen presentation and immune system activation. Antibodies or antagonists directed against these proteins may be useful in reducing or eliminating disorders associated with tumour necrosis factor (TMF) and TMF-like cytokines, such as endotoxic shock and autoimmune disorders and for treating infectious diseases including silicosis, sarcoidosis and idiopathic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotide encoding peptidoglycan recognition protein-like protein, antibodies specific to it useful for preventing, treating conditions e.g. endotoxic shock and auto-immune disorders and infections in mammal
                                                                                                                                                                                                                                                                                                                                      Sequence
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AAGACACTGGGCTGCGACGTGGGCTACAACTTCCTGATTGGAGAAGACGGGCTCGTA
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          This CDNA sequence encodes the precursor (see AAW23722) of a novel claimed antimicrobial peptide from bovine neutrophils, designated bovine granulocyte peptide A or BGP-A (see AAW23724). It was isolated from bovine bone marrow cDNA using PCR and RACE procedures. The encoded BGP-A precursor comprises a 21-amino acid
                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                           Claim 13; Fig
                                                                                                         Antimicrobial (poly)peptide(s) from bovine and murine useful therapeutically, as preservatives for food, in
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DB; AAW23722.
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A precursor comprises a 21-amino acid propeptide and 13 C-terminal amino
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                                                                                                                                                                                                                                                                            GlyArgGlyTrpAsnPheThrGlyAlaHisSerGlyHisLeuTrpAsnProMetSerIle
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                                                                                                                                                              GCCCAGAGTCTGCTGGCTTGTGGCGCAGCTCGGGGATACCTGACTCCTAACTACGAAGTC
                                                                                                                                                                             AlaGlnGlyLeuLeuAlaCysGlyValAlaGlnGlyAlaLeuArgSerAsnTyrValLeu
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Mouse tag7 clone coding sequence

18-MAY-1999

(first entry)

AAX21819

standard;

cDNA;

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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Georgiev
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melanoma; leukaemia; apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leukaemia
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             LysThrLeuGlyTrpCysAspValGlyTyrAsnPheLeuIleGlyGluAspGlyLeuVal
                                                                       SerCysAsnThrProAlaSerCysGlnGlnGlnAlaArgAsnValGlnHisTyrHisMet
                                                                                                              ATGTTGTTTGCCTGTGCTCCTTGCCCTCCTGGGTCTGGCAACCTCC------
AATGAGCTGGGCTGCGATGTAGCCTACAACTTCCTTATTGGAGAGGACGGTCATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              for isolating tag7 and therapeutically to inhibit or delay tumour
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67.20%
65.84%
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inducer; mouse; ds.
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Matches:
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                                                                                                                                                                                                                                                                                                                                                               fungicide; antiprotozoa; protozoacide;
murine granulocyte peptide A; MGP-A; pr
endotoxaemia; mouse; ss.
                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial
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                                                                                                  Antimicrobial (poly)peptide(s) from bovine and murine granulocytes useful therapeutically, as preservatives for food, in water
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                                                                         Claim 14; Fig 5;
                                                                                           treatment and in agriculture
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                                                                                                                               AAW23723.
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                                                                                                                                                                            CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                               peptide; antibiotic; antibacterial; antifungal;
tiprotozoa; protozoacide; antiviral; virucide;
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                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 36..581
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                                                                                                                                                                                                                                                                                                        /*tag=
                                                                         56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                           peptide A
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claimed antimicrobial peptide from bovine neutrophils, designated murine granulocyte peptide A or MGP-A (see AAW33725). It was isolated from murine bone marrow CDNA using primers based on bovine BGP-A CDNA (see AAT78509). The encoded MGP-A precursor comprises signal peptide and propeptide sequences followed by 12 C-terminal amino acids corresponding to mature MGP-A. MGP-A and

cDNA sequence encodes the precursor (see AAW23723)

designated of a novel,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BGP-A (see AAW23724), exhibit activity against Gram-positive and Gram-negative bacteria, fungi and viruses, specifically Staphylococcus aureus, Escherichia coli, Candida albicans, Salmonella typhimurium and C. neoformans (claimed). They can be used in human or veterinary medicine (particularly to treat disorders associated with lipopolysaccharides, e.g. sepsis and endotoxaemia) or as preservatives in food products or in water supplies (claimed). They can also be applied to crops to reduce post-harvest spoilage or expressed in transgenic plants to increase
           Human 5′
                                    01-FEB-2000
                                                            AAZ42549
                                                                                    AAZ42549
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                                                                                                                                                                                            ValLeuLysGlyHisArgAspValGlnArgThrLeuSerProGlyAsnGlnLeuTyrHis 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease
           EST isolated from
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61.70%
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          cDNA library
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CysAlaGlnHisLeuSerLeuProLeuArgTyrValValValSerHisThrAlaGlySer 60

TGCGCCCAGCACCTGAGCCTGCCCTTACGCTATGTGGTGGTATCGCACACGGCGGGCAGC

227

AspProAlaCysCysSerProIleValProArgAsnGluTrpLysAlaLeuAlaSerGlu ATGCTGCTTGCCTCGCCCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAA

107

GACCCGGCCTGCTGCAGCCCCATAGTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAG

167 40

108 41

48 21

168

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                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                               Query Match:
                                                                                                                                                                      Score:
                                                                                                                                                                                                                                                                       CC ANY65438 represent the EST-related proteins any control of the ANY65438 represent the EST-related proteins corresponding to ANA24265 to ANX65438 represent the EST-related proteins corresponding to ANA24265 to CC ANX63052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated CC regions (UTRs) and upstream regulatory regions which control the coloration, development stage, rate, and quantity of protein synthesis, as concern as stability of mRNA. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in forensic procedures to identify individuals, or in cliquents to procedures to identify individuals, or in cliquents from abnormal gene expression. The products may also be used in colorating from abnormal gene expression. The products may also be used in cused for directing extracellular secretion of a polypeptide can be conserved in the proteins encoded by the EST sequences may be useful in the acell. The proteins encoded by the EST sequences may be useful in the treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins is valuable. ANX42249 to ANZ4264 and ANY64644 to ANY64650 represent in the coloration of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dumas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human: 5' EST; expressed sequence tag; secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability; regulation; identification; ss.
                                                                                                                                                                                                                                                Sequence 380 BP; 67 A; 130 C; 114 G; 63 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ42265 to AAZ43075 represent novel 5' expressed sequence
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MetLeuLeuAlaTrpAlaLeuProSerLeuLeuArgLeuGlyAlaAlaGlnGluThrGlu
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98US-0069047
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96.40%
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US-09-462-625-4 (1-191) x ABL25881
                       Query Match:
DB:
                                               Percent Similarity:
Best Local Similarity:
                                                                                                 Alignment Scores:
                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLJ01840-ABLJ0175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 29116;
                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid genes from Drosophila and
                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                    No.:
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IleValProArgAsnGluTrpLysAlaLeuAlaSerGluCysAlaGlnHisLeuSerLeu

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention
                                           Claim 1; SEQ ID NO 29113; 21pp + Sequence Listing; English.
                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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11-JUL-2000;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                 1012
                                                                                                                                                                                                                                                                                                                                                                          1192
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nephrotropic; a cardiovascular
         Human; nootropic; neuroprotective; anticonvulsant; antidepressant; neuroleptic; tranquiliser; antiarrhythmic; cardiant; antiasthmatic antiinflammatory; antilipaemic; hepatotropic; virucide; antidiabet nephrotropic; anorectic; cytostatic; vaccine; neurological disease
                                                                             Human polynucleotide
                                                                                                                                                                                                                                                                     1072
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                                                                                                                                                            ABA90336 standard;
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                                                                                                                                                                                                                                                                                                                                         AlaCysGlyValAlaGlnGlyAlaLeuArgSerAsnTyrValLeuLysGlyHisArgAsp
                                                                                                                                                                                                                                                                                       ValGlnArgThrLeuSerProGlyAsnGlnLeuTyrHisLeuIleGlnAsnTrpProHis
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                                                                                                                                                                                                                                                                                                                   TCCGATGCGGTCAGTCGCGGCCAGATCGTTTCCGGATACATCCTGTACGGACATCGGCAG
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414.50
66.26%
47.24%
39.44%
23
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                                                                              #11
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respiratory disease;
                                                                                                                                                            726
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Indels:
Gaps:
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Conservative:
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                                      antiasthmatic;
                       antidiabetic;
           disease;
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4 AlaTrpAlaLeuProSerLeuLeuArg---

AGTTATGTTCAGCCACTTCTTGTGAAAGGCGAGAACTGCCTGGCCCCTCGGCAGAAGACA

-LeuGlyAlaAlaGlnGluThr

19

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Percent Similarity:
Best Local Similari
                                                                                                                                                                                      The invention relates to an isolated polypeptide comprising a 277, 480, CC 844, 782, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026, CC 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 619, 490, 462, 255, CC 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as CC given in the specification. The polypeptides, modulators of the C polypeptides and antibodies against the polypeptides are useful for C treating diseases such as neurological and psychiatric diseases CC including Alzhelmer's, parasupranuclear palsy, Huntington's disease, C myotonic dystrophy, anorexia and depression; cardiovascular diseases, CC including congestive heart failure, Hodgkin's disease and myocardial CC infarction; respiratory diseases including asthma, chronic obstructive CC pulmonary disease, cystic fibrosis and adult respiratory distress syndrome; liver diseases including hypercholesterolaemia, cirrhosis, CC viral and nonviral hepatitis, Type II diabetes mellitis, and impaired CC glucose tolerance; renal disease including renal failure, acute tubular CC excepts and glomerulomephritis; skeletal muscle diseases including CC diseases including myotonia congenita and intestinal obstruction; lymph (CC diseases including hyphagiactasia, diseases of placenta including chortocarcinoma; diseases of testes including testicular cancer, CC male reproductive diseases including low testosterone and male (CC Type 1 and 2 diabetes and obesity. The present sequence encodes a colveentide of the invention.
   US-09-462-625-4
                                              Query
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11-MAY-2000;
25-MAY-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polypeptides and polynucleotides useful as a vaccine for preventing and treating diseases associated the polypeptide, e.g. Alzheimer's disease, dyslipidemia, obesity, diabetes, infertility.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           renal disease; skeletal muscle disease; gastrointestinal disease; placental disease; testicular cancer; male fertility; pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                                                                                                                                                                                     polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Page 51; 116pp; English.
                                                              Similarity:
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Xie
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2000US-203336P.
2000US-207087P.
2000US-207546P.
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                              1.29e-33
413.00
62.11%
40.00%
39.30%
24
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(1-726)
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Matches:
Conservative:
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RESULT 14
AAD04006
Acquired Immune Deficiency Syndrome; epithelial infection; urinary tract; respiratory; vaginal; ovarian; rectal; chromosome 1; ss.
                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                              Human full length granulocyte peptide homolog Zgpal cDNA #2
              20-OCT-2000; 2000WO-US29177
                                                                           WO200129224-A2
                                                                                                                                  mat_peptide
                                                                                                                                                                sig_peptide
                                                                                                                                                                                                                                                                                                                                                                 vulnerary; dermatological;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValTyrGluGlyArgGlyTrpAsnPheThrGlyAlaHisSerGlyHisLeuTrpAsnPro 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ### ATAGACAGGCTCAAGTCATGCGACATTGGTTATAACTTCCTGGTGGGCCAGGATGGCGCC 453
                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACATCATCAGCACCTGGCCTCATTTCAAA 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HisLeuIleGlnAsnTrpProHisTyrArg 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACCTGCTGGTGGGCCACAGTGATGTGGCCCGAACCTTGTCTCCTGGGCAGGCTTTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrValLeuLysGlyHisArgAspValGlnArgThrLeuSerProGlyAsnGlnLeuTyr 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTAGAGGCAGCCCAAGACCTGATCCAGTGTGCCATGGTCAAAGGGTACCTGACTCCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleArgAlaAlaGlnGlyLeuLeuAlaCysGlyValAlaGlnGlyAlaLeuArgSerAsn 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTGCCCTGGGCATTACCTTCATGGGCACCTTCACAGGTATACCACCCAATGCTGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetSerIleGlyIleSerPheMetGlyAsnTyrMetAspArgValProThrProGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTATGAAGGGGTGGGCTGGAATGTCCAAGGCTCC---TCCACCCCTGGCTACGATGAC 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MetLysThrLeuGlyTrpCysAspValGlyTyrAsnPheLeuIleGlyGluAspGlyLeu 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGACCTGCAACATTTCTGATGAGTGCCGCCTGCTGGTCCGGGACATCCAGTCTTTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerSerCysAsnThrProAlaSerCysGlnGlnGlnAlaArgAsnValGlnHisTyrHis 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACTGTCCCAGG----ATGACTCTCCCAGCGAAGTATGGCATCATTATCCACACTGCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                granulocyte peptide A;
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                   52..1107
                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                       /product-
                                                                                                                     /*tag=
                                                                                                                                                 *tag=
                                                                                                                                                                               inker sequence"
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                                                                                                         "Mature
                                                                                                                                                                                                                                                                                                                                                               A; GP-A; Zgpal; cytostatic; antiinflammat anti-microbial; gastrointestinal disease;
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                                                                                                     human full length zgpal
                                                                                                                                                                                                                                                                                                                                    gene therapy; AIDS;
wound; cystic fibrosis;
                                                                                                                                                                                               protein
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CC peptide (GP-A) homolog, Zgpal protein. Zgpal gene is located on human CC chromosome 1. Zgpal polypeptides are useful for producing antibodies CC which are useful for detecting cancer. Zgpal polypeptides having CC anti-microbial activity are useful for treating dental carries, CC periodontal disease, thrush, gastrointestinal disease, urinary tract CC infections, respiratory infections, vaginal infections acquired immune CC deficiency syndrome (AIDS) and lung infections associated with cystic CC ibrosis and prevention of infection in skin and other epithelial wounds. CC Zgpal-cytokine fusion proteins are useful for enhancing in vivo killing CC ovarian and rectal cancers). Zgpal polypeptides, fragments, fusion CC proteins or agonists are useful in in vitro studies of exogenous CC microorganism infections such as bacterial, viral or fungal infection and CC also to study epithelial call defensin induction in cell culture. Zgpal antibodies, polynucleotides and polypeptides are useful for detection of CC zgpal polypeptide, mRNA or anti-zgpal antibodies, thus serving as markers for detecting genetic diseases or cancers. Zgpal sequences are useful as CC diagnostics in forensic DNA profiling and as probes or primers to clone councers. Signal gene is antibodies are useful for detection as concers. Zgpal sequences are useful as neutralizing antibodies or as antagonists to block zgpal activity in vitro and in vivo. Zgpal gene is also useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New granulocyte peptide homolog, zgpal polypeptide, for research applications, diagnosis and treatment of cancer, periodontal, gastrointestinal disease, urinary tract, skin and lung infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 107-109; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
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12-JUL-2000; 2000US-0218070.
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence is a cDNA encoding human full length
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1110
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B₽;
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249 A; 319
Ç
295 G;
  247
  Τ;
  0 other;
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Best Local Similarity: Query Match: Score: Alignment Pred. No.: Percent Similarity: 2.28e-33 413.00 62.11% 40.00% 39.30% 22 Mismatches: Indels: Matches: Conservative:

US-09-462-625-4 (1-191)* AAD04006 (1-1110)

Gaps:

837	778 ATAGACAGGCTCAAGTCATGCGACATTGGTTATAACTTCCTGGTGGGCCAGGATGGCGCC 837	778	ф
99	80 MetLysThrLeuGlyTrpCysAspValGlyTyrAsnPheLeuIleGlyGluAspGlyLeu 99	80	γQ
777	718 AGGACCTGCAACATTTCTGATGAGTGCCGCCTGCTGGTCCGGGACATCCAGTCTTTCTAC 777	718	В
79	ThrProAlaSerCysGlnGlnGlnAla	60	Qy
717	661 CACTGTCCCAGGATGACTCTCCCAGCGAAGTATGGCATCATTATCCACACTGCCGGG 717	661	DЪ
59	40 GluCysAlaGlnHisLeuSerLeuProLeuArgTyrValValValSerHisThrAlaGly 59	40	Qy
660	601 AGCCTGAAGAAGGCTTGCCCCGGCGTTGTCCCCACGGTCTGTGTGGGGAGCCAGGGAGACC 660	601	рb
39	20 GluAspProAlaCysCysSerProIleValProArgAsnGluTrpLysAlaLeuAlaSer 39	20	Qy
600	AGTTATGTTCAGCCACTTCTTGTGAAAGGCGAGAACTGCCTGGCCCCTCGG	. 541	Db
19	AlaTrpAlaLeuProSerLeuLeuArgLeuGlyAlaAlaGlnGluThr 19	4	Qγ

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11-MAY-2000;
25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; neuroprotective; anticonvulsant; antidepressant; neuroleptic; tranquiliser; antiarrhythmic; cardiant; antiasthmatic; antiinflammatory; antilipsemic; hepatotropic; virucide; antidiabetic; nephrotropic; anorectic; cytostatic; vaccine; neurological disease; cardiovascular disease; respiratory disease; liver disease; renal disease; skeletal muscle disease; gastrointestinal disease; placental disease; testicular cancer; male fertility; pancreatic disease;
The invention relates to an isolated polypeptide comprising a 277, 480, 583, 581, 628, 424, 638, 229, 310, 841, 241, 369, 382, 185, 586, 1026, 844, 782, 262, 394, 471, 485, 286, 533, 495, 350, 692, 462, 255, 784, 252, 593, 472, 607, 781, 640, 686 or 154 amino acid sequence as given in the specification. The polypeptides, modulators of the polypeptides and antibodies against the polypeptides are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1075
                                                                                                                                                                                                                                               asthma,
                                                                                                                                                                                                                                                                  Novel polypeptides and polynucleotides useful as a vaccine for preventing and treating diseases associated the polypeptide, e.g. altheomer's disease, dyslipidemia, obesity, diabetes, infertility,
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                                                                                                                                                                                           Claim 2; Page 51; 116pp;
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